

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 03:18:11 ; Search time 5462 Seconds

(without alignments)
11041.908 Million cell updates/sec

Title: US-10-826-929A-1

Perfect score: 1061

Sequence: 1 agcaaaagcaggggatatatt.....taccagaaaagcaaatcaga 1061

Scoring table: IDENTITY NUC
Gapop 10⁻⁷, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1061	100.0	1061	13	AF197241 Influenza
2	1056.2	99.5	1061	13	AY273168 Influenza
3	1053	99.2	1061	13	AF197248 Influenza
4	1051.4	99.1	1061	13	AF197247 Influenza
5	1048.2	98.8	1061	13	FLAH33
6	1043.4	98.3	1060	13	EIVV14059
7	1041.8	98.2	1060	13	EIVV14060
8	1041.8	98.2	1062	13	FLAH33
9	1039.2	97.9	1100	13	EIVV14058
10	1038.6	97.9	1762	13	FLAH33
11	1035.4	97.6	1061	13	AF197242
12	1033.8	97.4	1762	6	BD244631
13	1033.8	97.4	1762	6	AR254631
14	1033.8	97.4	1762	6	AR343239
15	1033.8	97.4	1762	6	AR455506
16	1033.8	97.4	1762	6	AR609062
17	1033.8	97.4	1762	13	FLAH33
18	1032.2	97.3	1762	6	BD244629

19	1032.2	97.3	1762	6	AR254629	AR254629 Sequence
20	1032.2	97.3	1762	6	AR343237	AR343237 Sequence
21	1032.2	97.3	1762	6	AR455504	AR455504 Sequence
22	1032.2	97.3	1762	6	AR609060	AR609060 Sequence
23	1030.6	97.1	1061	13	AF197245	AF197245 Influenza
24	1030.6	97.1	1762	13	FLAH33	L39917 Influenza A
25	1029	96.8	1061	13	AF197249	AF197249 Influenza A
26	1027.4	96.0	1762	13	FLAH33	L39915 Influenza A
27	1022.6	96.4	1061	13	AF197243	AF197243 Influenza A
28	1022.6	96.4	1061	13	AF197244	AF197244 Influenza A
29	1022.6	96.4	1090	13	EIVV14056	Y14056 Influenza A
30	1022.6	96.4	1762	13	IVAH691	X95637 Influenza A
31	1021.2	96.2	1762	13	IVAH991	X95638 Influenza A
32	1019.4	96.1	1061	13	AY273167	AY273167 Influenza A
33	1019.2	96.1	1032	13	IVTAN931	X85088 Influenza A
34	1019.2	96.1	1698	6	AR490205	AR490205 Sequence
35	1019.2	96.1	1698	6	AX018718	AX018718 Sequence
36	1018.4	96.0	1762	6	AR011427	AR011427 Sequence
37	1018.4	96.0	1762	6	I18065	I18065 Sequence 30
38	1016.8	95.8	1762	13	FLAH33	M24726 Influenza A
39	1016.2	95.8	1762	13	EIVH3A	L27597 Influenza A
40	1015.6	95.7	1040	13	FLAH33	D30680 Influenza A
41	1014.6	95.6	1061	13	AF197246	AF197246 Influenza A
42	1014.6	95.6	1762	13	AY855341	AY855341 Influenza A
43	1014.2	95.6	1099	13	FLAH33	D30681 Influenza A
44	1011.8	95.4	1093	13	FLAH33	M24728 Influenza A
45	1010.4	95.2	1762	13	FLAH33	M24728 Influenza A

ALIGNMENTS

RESULT 1

AF197241

LOCUS AF197241 1061 bp mRNA linear VRL 08-JAN-2003
DEFINITION Influenza A virus (A/equine/Kentucky/1/98 (H3N8)) hemagglutinin precursor (HA1) mRNA, partial cds.

ACCESSION AF197241

VERSION AF197241.1 GI:6651502

KEYWORDS

SOURCE Influenza A virus (A/equine/Kentucky/1/98 (H3N8))

ORGANISM Influenza A virus (A/equine/Kentucky/1/98 (H3N8))

Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

Influenzavirus A.

REFERENCE 1 (bases 1 to 1061)

Lai, A.C., Chambers, T.M., Holland, R.E. Jr., Morley, P.S.,

Haines, D.M., Townsend, H.G. and Barrandeguy, M.

Diverged evolution of recent equine-2 influenza (H3N8) viruses in

the Western Hemisphere

Arch. Virol. 146 (6), 1063-1074 (2001)

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

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REFERENCE

AUTHORS

TITLE

JOURNAL

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.5e-235;
Matches 1061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 301 GTGATCTCTCCAGTATGAAATGGAGCTCTTCATAGAAAGACAGCGCTTTCAGCA 360
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DB 361 ATTGCTACCCATATGACATCCCTGACTATGATCGCTCCGGTCCATTTAGCATCCTCAG 420
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DB 1021 TGGCCACTGGGATGAGGAATATACCAAGAAACCAATCAGA 1061

RESULT 2
AY273168
LOCUS
DEFINITION
Influenza A virus (A/equine/Oklahoma/2000(H3N8)) hemagglutinin
precursor (HA1) gene, partial cds.
ACCESSION
AY273168
VERSION
AY273168.1 GI:33415851
KEYWORDS
Influenza A virus (A/equine/Oklahoma/2000(H3N8))
Influenza A virus (A/equine/Oklahoma/2000(H3N8))
Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
REFERENCE
1 (bases 1 to 1061)
Lai, A.C.K., Rogers, K.M., Glaser, A., Tudor, L. and Chambers, T.
Alternate circulation of recent equine-2 influenza viruses (H3N8)
from two distinct lineages in the United States
Virus Res. 100 (2), 159-164 (2004)
PUBMED
15019234
REFERENCE
2 (bases 1 to 1061)
Lai, A.C.K.
Direct Submission
Submitted (10-APR-2003) Microbiology & Molecular Genetics, Oklahoma
State University, 306 Life Science East, Stillwater, OK 74078, USA
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gene
CDS
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ORIGIN

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Query Match 99.5%; Score 1056.2; DB 13; Length 1061;
Best Local Similarity 99.7%; Pred. No. 1.9e-234;
Matches 1058; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy	181	TGACAAATGCTACTGAAATTAGTTCAGAGCATTTCAATAGGGAATAATATGCAACAACTCAT	240
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Qy	241	ATAAAGTTCTAGATGGGAAGAAATTGCACTTAATAGATGCAATGCTAGGAGACCCCACT	300
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Qy	301	GTGATGCTTCCAGTATGAGAAATTTGGGACCTCTTCATAGAAGAAGCAGCGCTTTTCAGCA	360
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Qy	361	ATTGCTACCCCATATGACATCCCTGCACTATGTCATCGCTCGGTGCATTTGTAGCATCTCTCAG	420
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Qy	901	TTTGTGTGCTGTAATGTATTACCAAATGGAAGCATCCCCAACGACAAACCAATTTCAAA	960
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RESULT 3
AF197248
LOCUS

AF197248 1061 bp mRNA linear VRL 08-JAN-2003

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DEFINITION
Influenza A virus (A/equine/Kentucky/1/96 (H3N8)) hemagglutinin
precursor (HA1) mRNA, partial cds.
ACCESSION
AF197248
VERSION
AF197248.1 GI:6651516
KEYWORDS
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SOURCE
Influenza A virus (A/equine/Kentucky/1/96 (H3N8))
ORGANISM
Influenza A virus (A/equine/Kentucky/1/96 (H3N8))
Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
1 (bases 1 to 1061)
Lai, A.C., Chambers, T.M., Holland, R.E. Jr., Worley, P.S.,
Haines, D.M., Townsend, H.G. and Barrandeguy, M.
Diverged evolution of recent equine-2 influenza (H3N8) viruses in
the Western Hemisphere
Arch. Virol. 146 (6), 1063-1074 (2001)
11504416
2 (bases 1 to 1061)
Lai, A.C.K.
Direct Submission
Submitted (21-OCT-1999) Microbiology & Molecular Genetics, Oklahoma
State University, 306 Life Science East, Stillwater, OK 74078, USA
FEATURES
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Best Local Similarity 99.5%; Pred. No. 1e-233;
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Query Watch	99.2%;	Score 1053;	DB 13;	Length 1061;
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Db	181	TGACAAATGCTACTGAAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACACTCAT	240	
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Db	241	ATAGAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCACT	300
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QY	661	TCCAAGAAATCAGACAGTAACAGTCTCAACAAAAGAGTCAACAAACGATAGTCCCTA	720
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RESULT 4	AF197247	AF197247	1061 bp	mRNA	linear	VRL 08-JAN-2003
LOCUS	Influenza A virus (A/equine/kentucky/9/95 (H3N8))	precursor (HAI) mRNA, partial cds.				hemagglutinin
DEFINITION	AF197247					
ACCESSION	AF197247					
VERSION	AF197247.1	GI:6651514				
KEYWORDS	Influenza A virus (A/equine/kentucky/9/95 (H3N8))					
SOURCE	Influenza A virus (A/equine/kentucky/9/95 (H3N8))					
ORGANISM	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.					
REFERENCE	1 (bases 1 to 1061)					
AUTHORS	Lai, A.C., Chambers, T.M., Holland, R.E. Jr., Morley, P.S., Haines, D.M., Townsend, H.G. and Barrandeguy, M.					
TITLE	Diverged evolution of recent equine-2 influenza (H3N8) viruses in the Western Hemisphere					

JOURNAL	Arch. Virol. 146 (6), 1063-1074 (2001)
PUBMED	11504416
REFERENCE	2 (bases 1 to 1061)
AUTHORS	Lai, A.C.K.
TITLE	Direct Submission
JOURNAL	Submitted (21-OCT-1999) Microbiology & Molecular Genetics, Oklahoma State University, 306 Life Science East, Stillwater, OK 74078, USA
FEATURES	Location/Qualifiers
Source	1..1061
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	/gene="HA1"
CDS	30..>1061
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	/protein_id="AAF22351.1"
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sig_peptide	30..74
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mat_peptide	75..>1061
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ORIGIN

Query Match	99.1%	Score 1051.4;	DB 13;	Length 1061;
Best Local Similarity	99.4%;	Pred. No. 2.5e-233;		
Matches 1055;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	1	AGCAAAAGCAGGGGATATTTCTGTCATCATGAAGACAAACCACTATTTTGTACTACTGA	60	
Db	1	AGCAAAAGCAGGGGATATTTCTGTCATCATGAAGACAAACCACTATTTTGTACTACTGA	60	
QY	61	CCCATTTGGTCTACAGTCAAAACCCCAACCCAGTGGAAACAAACACAGCCACATTATGCTGG	120	
Db	61	CCCATTTGGTCTACAGTCAAAACCCCAACCCAGTGGAAACAAACACAGCCACATTATGCTGG	120	
QY	121	GAACCATCGAGTAGCAAAATGGAACATTTGGTAAACAAATACTGATGACCAAAATTGAGG	180	
Db	121	GAACCATCGAGTAGCAAAATGGAACATTTGGTAAACAAATACTGATGACCAAAATTGAGG	180	
QY	181	TGACAAATGCTACTGAAATTTAGTTCAGAGCATTTCAATAGGAAATATGCAACAATCAT	240	
Db	181	TGACAAATGCTACTGAAATTTAGTTCAGAGCATTTCAATAGGAAATATGCAACAATCAT	240	
QY	241	ATAAAGTTCTAGATGGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT	300	
Db	241	ATAAAGTTCTAGATGGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT	300	
QY	301	GTGATGCTTCCAGTATGAGAATTTGGGACCTCTTCTATAGAAAGACAGCGCTTTCAGCA	360	
Db	301	GTGATGCTTCCAGTATGAGAATTTGGGACCTCTTCTATAGAAAGACAGCGCTTTCAGCA	360	
QY	361	ATTGCTACCCATATGACATCCCTGACTATGCAATGCTCCGGTCCATTTAGCATCCTCAG	420	
Db	361	ATTGCTACCCATATGACATCCCTGACTATGCAATGCTCCGGTCCATTTAGCATCCTCAG	420	
QY	421	GAACATTAGAAATTCACAGCAGAGGGATTCACATGGACAGGTGTCTCAAAACGGAAGAA	480	
Db	421	GAACATTAGAAATTCACAGCAGAGGGATTCACATGGACAGGTGTCTCAAAACGGAAGAA	480	

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QY 481 GTGGAGCCTGCAGAAAGGGATCAGCGATAGTTCTTTAGCCGACTGAATTCGCTACAA 540
Db 481 GTGGAGCCTGCAGAAAGGGATCAGCGATAGTTCTTTAGCCGACTGAATTCGCTACAA 540
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Db 601 AACTATACATCTGGGGATTCATCACCAGGCTCAACCAACCAACAGCAGCAGAAATTTGACA 660
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Db 721 ATATCGGATCTAGACCGTGGGTAGGGTCAATCAGGAGGATTAAGCATATCTGGACCA 780
QY 781 TTGTAAACCTGGAGATCTCTAATGATAACAGTAAATGSCAACTTAGTTGCACCGCGG 840
Db 781 TTGTAAACCTGGAGATCTCTAATGATAACAGTAAATGSCAACTTAGTTGCACCGCGG 840
QY 841 GATATTTTAAATGAAAACAGGAAAGCTCTGTAAATGAGATCAGATGCAACCCATAGACA 900
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Db 901 TTTGTGTCTGATGATTAACCAAAATGGAAGCATCCCAACGACAAACCACTTTTCAA 960
QY 961 ATGTGAACAAATGATGAAATGCCCAGGATATATCAGGCAAAAACCTTTAAAGC 1020
Db 961 ATGTGAACAAATGATGAAATGCCCAGGATATATCAGGCAAAAACCTTTAAAGC 1020
QY 1021 TGGCCACTGGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061
Db 1021 TGGCCACTGGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061

RESULT 5
FLAH3B 1762 bp ss-RNA linear VRL 01-NOV-2004
LOCUS Influenza A virus (A/equine/kentucky/1/94 (H3N8)) hemagglutinin
DEFINITION precursor (HA) gene, complete cds.
ACCESSION L39914
VERSION L39914.1 GI:722403
KEYWORDS Influenza A virus (A/equine/Kentucky/1/94 (H3N8))
SOURCE Influenza A virus (A/equine/Kentucky/1/94 (H3N8))
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
REFERENCE 1 (bases 1 to 1762)
AUTHORS Daly J.M., Lai, A.C., Binns, M.M., Chambers, T.M., Barrandeguy, M. and
Mumford, J.A.
TITLE Antigenic and genetic evolution of equine H3N8 influenza A viruses
JOURNAL J. Gen. Virol. 77 (pt 4), 661-671 (1996)
PUBMED 8627254
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/gene="HA"

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ORIGIN

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Matches 1053; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 61 CCCATTGGGCTACAGTCAAAACCCCAACCAAGTGGAAACACACAGCCACATTATGCTGG 120
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Db 121 GACACCATGAGTAGCAAAATGGAACATTTGGTAAAAACAATACTGATGACCAAAATTGAGG 180
QY 181 TGACAAATGCTACTGATTAATGTTTACAGAGCATTTTCAATAGGGAATAATGCAACCACTCAT 240
Db 181 TGACAAATGCTACTGATTAATGTTTACAGAGCATTTTCAATAGGGAATAATGCAACCACTCAT 240
QY 241 ATAAAGTTCTAGATGGAAGAAATTTGACACATTAATAGATGCAATGCTAGGAGACCCCACT 300
Db 241 ATAGAGTTCTAGATGGAAGAAATTTGACACATTAATAGATGCAATGCTAGGAGACCCCACT 300
QY 301 GTGATGCTTCAGTATGAGAAATTTGGACCTCTTTCATAGAAAGACAGCGCTTTTACGCA 360
Db 301 GTGATGCTTCAGTATGAGAAATTTGGACCTCTTTCATAGAAAGACAGCGCTTTTACGCA 360
QY 361 ATTGCTACCATATGATCCCTGATGATGATGCTCGCTCGCTCCATTTGTAGCATCTCTCAG 420
Db 361 ATTGCTACCATATGATCCCTGATGATGATGCTCGCTCGCTCCATTTGTAGCATCTCTCAG 420
QY 421 GAACATTAGAAATTTACAGCAGAGGGATTTACATGAGCAGGTTGCTCAAAAACGGAAGAA 480
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QY 601 AACTATACATCTGGGGATTCATCACCAGGCTCAACCAACCAACAGCAGCAGAAATTTGACA 660
Db 601 AACTATACATCTGGGGATTCATCACCAGGCTCAACCAACCAACAGCAGCAGAAATTTGACA 660
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LOCUS      FLAHA3D      1762 bp ss-RNA      linear      VRL 01-NOV-2004
DEFINITION Influenza A virus (A/equine/Florida/1/93 (H3N8)) hemagglutinin
 precursor (HA) gene, complete cds.
ACCESSION  L39916
VERSION     L39916.1      GI:722407
KEYWORDS
ORGANISM    Influenza A virus (A/equine/Florida/1/93 (H3N8))
SOURCE      Influenza A virus (A/equine/Florida/1/93 (H3N8))
ORGANISM    Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
REFERENCE   1 (bases 1 to 1762)
AUTHORS     Daly,J.M., Lai,A.C., Binns,M.M., Chambers,T.M., Barrandeguy,M. and
            Mumford,J.A.
TITLE       Antigenic and genetic evolution of equine H3N8 influenza A viruses
JOURNAL     J. Gen. Virol. 77 (Pt 4), 661-671 (1996)
PUBMED      8627254
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sig_peptide
mat_peptide
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Best Local Similarity 98.9%; Pred. No. 3.7e-231;
Matches 1049; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY 61 CCCATTGGGTCTACAGTCAAAACCCACCACTGGAACACACAGCCACATTATGCTGG 120
Db 61 CCCATTGGGTCTACAGTCAAAACCCACCACTGGAACACACAGCCACATTATGCTGG 120
QY 121 GACACCATGAGTAGCAAAATGGAACTTGTGTAACCAATAAATCTGATGACCAAAATGAGG 180
Db 121 GACACCATGAGTAGCAAAATGGAACTTGTGTAACCAATAAATCTGATGACCAAAATGAGG 180
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181 TGACAAATGCTACTGAATAGTTAGTCAGAGCATTTCAATAGGAAAAATATGCAACACTCAT 240
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241 ATAGAGTTCTAGATGGAAGAAATTCACATTAAATAGATCAATGCTAGAGAGACCCCACT 300
301 GTGATGTCCTCCAGTATGAGAAATTTGGGACCTCTCTCATAGAAAGAGCAGCGCTTTGAGCA 360
301 GTGATGTCCTCCAGTATGAGAAATTTGGGACCTCTCTCATAGAAAGAGCAGCGCTTTGAGCA 360
361 ATTGCTACCATATGACATCCCTGACTATGCAATGCGTCCGCTCCATTTAGCATCTCTCAG 420
361 ATTGCTACCATATGACATCCCTGACTATGCAATGCGTCCGCTCCATTTAGCATCTCTCAG 420
421 GAACATTAGAAATTCACAGCAGAGGAAATTCACATGGACAGGTGTCACTCAAAACGGAGAA 480
421 GAACATTAGAAATTCACAGCAGAGGAAATTCACATGGACAGGTGTCACTCAAAACGGAGAA 480
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721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGCGAGGATAAGCATATATCTGACCA 780
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841 GATATTTTAAATTTGAAAAACAGGAAAAAGCTCTGTAAATGAGATCAGATGCAACCATAGACA 900
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901 TTGTGTGTCGATGATGATTTACACCAATGGAAGCATCCCCACGACCAACCACTTTTCAA 960
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961 ATGTGAAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTTAAAGC 1020
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1021 TGSCCACTGGGATGAGGAATATACCAAGAAAGCAAAATCAGA 1061

RESULT 9
EIVY14058
LOCUS
DEFINITION Influenza A virus (A/equi 2/Soderala/94 (H3N8)) gene for
hemagglutinin HA1 subunit, isolate A/equi 2/Soderala/94.
Y14058
Y14058.1 GI:2765369
VERSION hemagglutinin HA1 subunit.
KEYWORDS Influenza A virus (A/equi 2/Soderala/94 (H3N8))
SOURCE Influenza A virus (A/equi 2/Soderala/94 (H3N8))
ORGANISM Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
REFERENCE 1 (bases 1 to 1100)
AUTHORS Oxburgh,L., Akerblom,L., Fridberger,T., Klingeborn,B. and Linne,T.

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TITLE Identification of two antigenically and genetically distinct lineages of H3N8 equine influenza virus in Sweden
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1100)
 AUTHORS Oxburgh, L.H.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-1997) Oxburgh L.H., Veterinary Microbiology, Swedish University of Agricultural Sciences, Biomedical Centre Box 585, s-751 23 Uppsala, SWEDEN
 FEATURES Location/Qualifiers
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 Best Local Similarity 98.8%; Pred. No. 1.7e-230;
 Matches 1047; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 2 GCAAAAGCAGGGGATATTTCTGTCATCATGAGCAACCACTATTATTTGATCTACTGAC 61
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 DB 62 CCATTGGTGTACAGTCAAAACCCCAATCAGTGGGCAACAACAGCCACATTTATGCTGGG 121
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 DB 362 TTGCTACCCATATGACATCCCTGACTATGATCGCTCGGTCCATTGTAGCATCCTTAGG 421
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Db 422 AACATTGGAATTCACAGCAGAGGGGATTCATCATGACAGGTTGTCATCTCAAAACCGGAAGA 481
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 LOCUS Influenza A virus (A/equine/Kentucky/1/91 (H3N8)) hemagglutinin
 DEFINITION precursor L39918
 ACCESSION L39918
 VERSION L39918.1 GI:722411
 KEYWORDS Influenza A virus (A/equine/Kentucky/1/91 (H3N8))
 SOURCE Influenza A virus (A/equine/Kentucky/1/91 (H3N8))
 ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 Influenzavirus A.
 REFERENCE 1 (bases 1 to 1762)
 AUTHORS Daly, J.M., Lai, A.C., Binns, M.M., Chambers, T.M., Barrandeguy, M. and Mumford, J.A.
 TITLE Antigenic and genetic evolution of equine H3N8 influenza A viruses
 JOURNAL J. Gen. Virol. 77 (Pt 4), 661-671 (1996)
 PUBMED 8627254
 FEATURES Location/Qualifiers
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sig_peptide

mat_peptide

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ORIGIN

Query Match 97.9%; Score 1038.6; DB 13; Length 1762;
Best Local Similarity 98.7%; Pred. No. 2.1e-230;
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DB 1021 TGGCCACTGGGATGAGGATATATACAGAAAAAGCAAAATCAGA 1061

RESULT 11
AF197242
LOCUS
DEFINITION
Influenza A virus (A/equine/Florida/1/94 (H3N8)) hemagglutinin precursor (HA1) mRNA, partial cds.
ACCESSION
AF197242
VERSION
AF197242.1 GI:6651504
KEYWORDS
Influenza A virus (A/equine/Florida/1/94 (H3N8))
Influenza A virus (A/equine/Florida/1/94 (H3N8))
Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
REFERENCE
1 (bases 1 to 1061)
Lai A.C., Chambers, T.M., Holland, R.E. Jr., Morley, P.S.,
Haines D.M., Townsend, H.G. and Barrandeguy, M.
Diverged evolution of recent equine-2 influenza (H3N8) viruses in
the Western Hemisphere
Arch. Virol. 146 (6), 1063-1074 (2001)
11504416
REFERENCE
2 (bases 1 to 1061)
Lai, A.C.K.
Direct Submission
Submitted (21-OCT-1999) Microbiology & Molecular Genetics, Oklahoma
State University, 306 Life Science East, Stillwater, OK 74078, USA
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ORIGIN

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Matches 1045; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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RESULT 12
BD244631
LOCUS
DEFINITION Low temperature-adaptable equine influenza virus.
ACCESSION BD244631
VERSION BD244631.1 GI:33054401
KEYWORDS JP 2002522078-A/7.
SOURCE Equine influenza virus H3N8
ORGANISM Equine influenza virus H3N8
Viruses; serNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
REFERENCE 1 (bases 1 to 1762)
AUTHORS Dowling,P.W. and Youngner,J.S.
TITLE Low temperature-adaptable equine influenza virus
JOURNAL Patent: JP 2002522078-A 7 23-JUL-2002;
THE UNIVERSITY OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER
EDUCATION
COMMENT OS Equine influenza virus H3N8
PN JP 2002522078-A/7
PD 23-JUL-2002
PF 12-AUG-1999 JP 2000565137
PR 13-AUG-1998 US 09/133921
PI PATRICIA W DOWLING,JULIUS S YOUNGNER
PC C12N15/09,A61K39/145,A61P31/16,C07K14/11,C12N7/04//C12N7/04,
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CC Low temperature-adaptable equine influenza virus PH Key
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ORIGIN

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RESULT 13
AR254631
LOCUS 1762 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 10 from patent US 6482414.
ACCESSION AR254631
VERSION AR254631.1 GI:27303652
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1762)
AUTHORS Dowling, P. W. and Youngner, J. S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6482414-A 10 19-NOV-2002;
The University of Pittsburgh-of the Commonwealth System of Higher
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Best Local Similarity 98.4%; Pred. No. 2.7e-229;
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DEFINITION Sequence 10 from patent US 6579528.
ACCESSION AR343239
VERSION AR343239.1 GI:33738757
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 1762)
AUTHORS Dowling, P.W. and Youngner, J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6579528-A 10 17-JUN-2003;
  The University of Pittsburgh - of the Commonwealth System of Higher
  Education; Pittsburgh, PA
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ORIGIN
Query Match 97.4%; Score 1033.8; DB 6; Length 1762;
Best Local Similarity 98.4%; Pred. No. 2.7e-229;
Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Db 961 ATGTGAACAAAGTTACATATGGAATAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
QY 1021 TGGCCACTGGGATGAGGAAATATACCAAGAAAGCAAAATCAGA 1061
Db 1021 TGGCCACTGGGATGAGGAAATATACCAAGAAAGCAAAATCAGA 1061

RESULT 15
LOCUS AR455506 1762 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 10 from patent US 6685946.
ACCESSION AR455506
VERSION AR455506.1 GI:42690326
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 1762)
AUTHORS Dowling, P.W. and Youngner, J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6685946-A 10 03-FEB-2004;
  The University of Pittsburgh-of the Commonwealth System of Higher
  Education; Pittsburgh, PA
FEATURES
  source 1..1762
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ORIGIN
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Best Local Similarity 98.4%; Pred. No. 2.7e-229;
Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Db 61 CCCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGAAACAACAGCCACATTTATGTCGG 120
QY 121 GACACCATGAGTAGCAATGGAACATTTGGTAAACCAATACATGATGACCAATTCAGG 180
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Qy	1021	TGGCCACTGGGAATGAGGAATATACGAGAAAGCAAAATCAGA	1061
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 23:58:01 ; Search time 678 Seconds
(without alignments)
10429.556 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1061	100.0	1061	14	Adw87317 Equine-2
2	1033.8	97.4	1762	3	Aaz50976 Cold-adap
3	1032.2	97.3	1762	3	Aaz50975 Wild type
4	1019.2	96.1	1698	2	Aaz30213 Sequence
5	1018.4	96.0	1762	2	Aaz30212 Sequence
6	987.4	93.1	1788	1	Aan71067 Equine HA (A
7	987.4	93.1	1797	2	Aan71067 Sequence
8	984	92.7	1698	3	Aaz30211 Sequence
9	984	92.7	1698	3	Aaz47007 Equine in
10	976.2	92.0	1762	2	Aaz30211 Equine HA (A
11	947.2	89.3	1698	2	Aav49391 EIV Fonta
12	607.2	57.2	1777	2	Aaz72855 Full leng
13	601.6	56.7	1765	6	Aba93937 Influenza
14	598.4	56.4	1764	6	Aba93944 Influenza
15	585.6	55.2	1762	1	Aan70642 Sequence
16	579.2	54.6	1762	14	Ady27535 Hemagglut
17	574.4	54.1	1762	14	Ady27539 Hemagglut
18	569.6	53.7	1755	14	Ady27533 Hemagglut
19	568	53.5	1762	14	Ady27541 Hemagglut

20	566.4	53.4	1762	14	ADY27537	Ady27537 Hemagglut
21	566.2	53.4	1091	6	ABQ82724	Abq82724 Influenza
22	564.8	53.2	1745	14	ADY27531	Ady27531 Hemagglut
23	558.2	52.6	1653	6	ABQ82723	Abq82723 Influenza
24	556	52.4	987	6	ABQ82725	Abq82725 Influenza
25	554.4	52.3	987	6	ABQ82725	Abq82725 Influenza
26	549.2	51.8	1793	2	AAT59212	Aat59212 Influenza
27	549.2	51.8	1793	2	AAT59212	Aat59212 Influenza
28	549.2	51.8	1793	5	AAD09586	Aad09586 Influenza
29	546.4	51.5	988	12	ADOL5237	Adol5237 Influenza
30	544.4	51.3	1757	2	AAT59216	Aat59216 Influenza
31	544.4	51.3	1757	2	AAO00777	Aao00777 Influenza
32	544.4	51.3	1757	5	AAD09590	Aad09590 Influenza
33	541.2	51.0	1701	2	AAV49298	Aav49298 SIV strai
34	541.2	51.0	1757	2	AAT59219	Aat59219 Influenza
35	541.2	51.0	1757	2	AAO00780	Aao00780 Influenza
36	541.2	51.0	1757	5	AAD09593	Aad09593 Influenza
37	150.4	14.2	1809	1	AAN71066	Aan71066 Sequence
38	150.4	14.2	1809	2	AAQ04596	Aaq04596 Equine he
39	148.2	14.0	1759	2	AAQ29110	Aaq29110 EIV HA (A
40	133.4	12.6	2005	3	AAA75002	Aaa75002 Nucleotid
41	133.4	12.6	4610	3	AAA75005	Aaa75005 Nucleotid
42	133.4	12.6	4930	3	AAA75000	Aaa75000 Nucleotid
43	127.2	12.0	1721	2	ADH29821	Adh29821 Swinepox
44	127.2	12.0	1721	2	AAV26247	Aav26247 Genomic D
45	125.2	11.8	1711	6	AAL50113	Aal50113 Recombina

ALIGNMENTS

RESULT 1

ADW87317
ID ADW87317 standard; DNA; 1061 BP.

XX AC ADW87317;

XX DT 21-APR-2005 (first entry)

XX DE Equine-2 influenza virus hemagglutinin protein HA1 coding sequence.

XX KW immunostimulant; vaccine; immunization; hemagglutinin; gene; ds.

XX OS Influenza virus.

XX FH Key Location/Qualifiers
FT CDS 30..1061

FT FT /*tag= b

FT FT /product= "hemagglutinin"

FT FT /note= "no stop codon given"

FT FT /transl_except= (pos:369..377,aa:ProApp)

FT FT /note= "a one codon insertion alters the reading frame"

FT FT sig_peptide 30..74

FT FT mat_peptide 75..1061

FT FT /*tag= c

XX US2005032732-A1.

XX 10-FEB-2005.

XX PF 16-APR-2004; 2004US-00826929.

XX PR 15-MAY-2003; 2003US-0470843P.

XX PA (LAI/A/) LAI A.

XX PI Lai A;

XX XX WPI; 2005-151686/16.

XX DR P-PSDB; ADW87316.

XX DR GENBANK; AF197241.

XX XX

CC encoding cold-adapted equine influenza virus H3N8 haemagglutinin (HA)
 CC protein denoted as PeiwhA565. This sequence is a modified form of the
 CC wild type sequence
 XX
 SQ Sequence 1762 BP; 641 A; 333 C; 381 G; 407 T; 0 U; 0 Other;
 Query Match 97.4%; Score 1033.8; DB 3; Length 1762;
 Best Local Similarity 98.3%; Pred. No. 1.4e-281;
 Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGATATTTCTGTCAATCATGAAGACCAACCATTTTGTACTACTGA 60
 Db 1 AGCAAAAGCAGGGATATTTCTGTCAATCATGAAGACCAACCATTTTGTACTACTGA 60
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 Db 61 CCCATTGGGTCTACAGTCAAAACCCCAACCACTGGAACCAACACAGCCACATTATGTCTGG 120
 QY 121 GACACCATGCAATGCAAAATGGAACATTTGGTAAACCAATTAACCTGATGACCAAAATTGAGG 180
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 QY 781 TTGTAAACCTGGAGATATCTTAATGATAACAGTAAATGCAACTTGTGACCGCGGG 840
 Db 781 TTGTAAACCTGGAGATATCTTAACGATAAACAGTAAATGCAACTTGTGACCGCGGG 840
 QY 841 GATATTTAAATTCAAAACAGGAAAGCTCTGTAAATGAGATCAGATGACACCATAGACA 900
 Db 841 GATATTTAAATTCAAAACAGGAAAGCTCTGTAAATGAGATCAGATGACACCATAGACA 900
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QY 961 ATGTGAACAAAGTTACATATGGAATGCCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
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 QY 1021 TGGCCACTGGGATGAGGAATATACAGAAAGCAAAATCAGA 1061
 Db 1021 TGGCCACTGGGATGAGGAATGATACCAAGAAAGCAAAATCAGA 1061

RESULT 3
 AAZ50975
 ID AAZ50975 standard; DNA; 1762 BP.
 XX
 AC AAZ50975;
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE Wild type equine influenza virus H3N8 haemagglutinin protein DNA.
 XX
 KW Haemagglutinin protein; wild type HA protein; horse; cold-adaptation;
 KW reassortant virus; temperature sensitivity; dominant interference;
 KW attenuation; antiviral; vaccine; prevention; treatment;
 KW influenza A virus infection; ds.
 XX
 OS Equine influenza virus H3N8.
 XX
 FH Key Location/Qualifiers
 CDS 30..1727
 FT /*tag= a
 FT /product= "HA protein"
 FT /note= "The coding region without the stop codon is
 FT specifically claimed"
 XX
 PN WO200009702-A1.
 XX
 XX 24-FEB-2000.
 XX
 PF 12-AUG-1999; 99WO-US018583.
 XX
 PR 13-AUG-1998; 98US-00133921.
 XX
 PA (UVP1-) UNIV PITTSBURGH.
 XX
 XX Dowling PW, Youngner JS;
 PI
 XX WPI; 2000-224339/19.
 DR P-PSDB; AAY70056.
 XX
 PT New cold-adapted equine influenza viruses and reassortant viruses used as
 PT vaccines for treating influenza infections in animals, particularly
 PT horses, have a phenotype such as temperature sensitivity or dominant
 PT interference.
 XX
 Claim 8; Page 82-85; 127pp; English.
 PS
 XX
 CC The patent discloses experimentally generated cold-adapted equine
 CC influenza viruses, and reassortant influenza A viruses comprising at
 CC least one genome segment of the cold-adapted virus, which confers at
 CC least one identifying phenotype selected from cold-adaptation,
 CC temperature sensitivity, dominant interference and attenuation. These
 CC viruses are used in therapeutic compositions e.g. vaccines for preventing
 CC or treating infections caused by influenza A viruses in animals,
 CC particularly horses. The present sequence is a DNA (neiwHA1762) encoding
 CC wild type equine influenza virus H3N8 haemagglutinin (HA) protein denoted
 CC as PeiwhA565. This sequence is modified to generate cold-adapted equine
 CC influenza virus
 XX
 SQ Sequence 1762 BP; 639 A; 334 C; 383 G; 406 T; 0 U; 0 Other;

Query Match 97.3%; Score 1032.2; DB 3; Length 1762;
 Best Local Similarity 98.3%; Pred. No. 3.9e-281;
 Matches 1043; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAAGACAACCATTTATTTGATACTACTGA 60
 Db 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAAGACAACCATTTATTTGATACCCTGA 60
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 Db 61 CCCATTGGGTCTACAGTCAAAACCCCAACAGTGGCAACAACACAGCCACATTATGTCGG 120
 QY 121 GACACATGAGTACAAATTTGGTAAACATTTGTAACCAATTAATCTGATGATGACCAATTTGAGG 180
 Db 121 GACACATGAGTACAAATTTGGTAAACATTTGTAACCAATTAATCTGATGATGACCAATTTGAGG 180
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 Db 181 TGCAAAATGCTAGTAAATTTGTCAGAGCATTTCAATAGGGAATATGCAACAACTCAT 240
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 Db 241 ATAGAGTTCTAGATGGAAGAAATTTGCACATTTAATAGATGCAATGCTAGGAGACCCCACT 300
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 Db 301 GTGATGCTTCCAGTATGAGAAATTTGGACCTCTTCAATAGAAAGACAGCGCTTTTCAGCA 360
 QY 361 ATTGCTACCCATATGACATCCCTGACTATGTCATGCTCCGGTCCATTTGATGATCCTCAG 420
 Db 361 GTTGCTACCCATATGACATCCCTGACTATGTCATGCTCCGGTCCATTTGATGATCCTCAG 420
 QY 421 GAA CATTAGAAATTTACAGCAGAGGGATTTCACTGAGCAGGTGTCTCAAAACGGAAGAA 480
 Db 421 GAACATTTGGAATTTACAGCAGAGGGATTTCACTGAGCAGGTGTCTCAAAACGGAAGAA 480
 QY 481 GTGAGCGCTGCAAAAGGGATGACGCGATAGTTCTTTAGCCGACTGAATTTGCTTAACAA 540
 Db 481 GTGAGCGCTGCAAAAGGGATGACGCGATAGTTCTTTAGCCGACTGAATTTGCTTAACAG 540
 QY 541 AATCTGGAACCTCTTACCCACATTTGAATGTGCAATGCTCAACATAAATAATTTTCGACA 600
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 QY 601 AACTATACATCTGGGGATTTCACTACCCGAGCTCAAAACAGCAGAGCAAGAAATTTGTACA 660
 Db 601 AACTATACATCTGGGGATTTCACTACCCGAGCTCAAAACAGCAGAGCAAGAAATTTGTACA 660
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 Db 661 TCCAAGATCAGACGAGTAAAGTCTCAACAAAAGAGTCAACAAACGATAGTCCCTA 720
 QY 721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGCAGGATAAGCATATCTGGACCA 780
 Db 721 ACATCGGATCTAGACCGGTTAGGGGTCAATCAGCAGGATAAGCATATCTGGACCA 780
 QY 781 TTGTAAACCTGAGATATCTTAATGATAACAGTAATGGCAACTTAGTTTGCACCGCGGG 840
 Db 781 TTGTAAACCTGAGATATCTTAATGATAACAGTAATGGCAACTTAGTTTGCACCGCGGG 840
 QY 841 GATATTTTAAATTTGAAAACAGGGAAGTCTCTGTAATGAGATCAGATGACCCATAGACA 900
 Db 841 GATATTTTAAATTTGAAAACAGGGAAGTCTCTGTAATGAGATCAGATGACCCATAGACA 900
 QY 901 TTTGTGTCTGATGATTTATACCAATGGAAGCATCCCCAAGCAACCACTTTTCAAA 960
 Db 901 TTTGTGTCTGATGATTTATACCAATGGAAGCATCCCCAAGCAACCACTTTTCAAA 960
 QY 961 ATGTGAACAAAGTTTACATATGGAATTTGCCCCAAGTATATCAGGCAAAACACCTTTAAAGC 1020
 Db 961 ATGTGAACAAAGTTTACATATGGAATTTGCCCCAAGTATATCAGGCAAAACACCTTTAAAGC 1020
 QY 1021 TGCCCACTGGATGAGGAATATACCAAGCAAAAGCAATTCAGA 1061
 Db 1021 TGCCCACTGGATGAGGAATATACCAAGCAAAAGCAATTCAGA 1061

RESULT 4
 AAZ30213
 ID AAZ30213 standard; DNA; 1698 BP.
 XX
 AC AAZ30213;
 XX
 DT 11-FEB-2000 (first entry)
 XX
 DE Sequence of the haemagglutinin (HA) gene of EIV strain Kentucky 1/94.
 XX
 KW Haemagglutinin gene; EIV; strain Kentucky 1/94; DNA vaccine; horse;
 KW acrylic acid polymer; methacrylic acid polymer; copolymer;
 KW maleic anhydride; alkenyl derivative; animal vaccine; viral infection;
 KW bacterial infection; ss.
 XX
 OS Equine influenza virus.
 XX
 PN FR2776928-A1.
 XX
 PD 08-OCT-1999.
 XX
 PF 03-APR-1998; 98PR-00004409.
 XX
 PR 03-APR-1998; 98PR-00004409.
 XX
 PA (MERI-) MERIAL SAS.
 XX
 PI Audonnet JCF, Minke JM;
 XX
 DR WPI; 1999-593389/51.
 XX
 PT Vaccine containing naked DNA and acrylic acid polymer or maleic anhydride
 PT copolymer, for protection against viral or bacterial diseases in animals.
 XX
 PS Example 9; Fig 2; 34pp; French.
 XX
 CC The present sequence represents the haemagglutinin gene of Equine
 CC influenza virus (EIV) strain Kentucky 1/94. The sequence was used to
 CC prepare a DNA vaccine for horses, representative of the DNA vaccines of
 CC the invention. The specification describes a DNA vaccine that comprises
 CC naked DNA encoding an antigenic polypeptide, and at least one adjuvant
 CC that is an acrylic or methacrylic acid polymer or a copolymer of maleic
 CC anhydride with an alkenyl derivative. The vaccines are simple and easy to
 CC prepare (simply by mixing components) and they do not involve any strong
 CC interactions between DNA and other components that are likely to cause
 CC complex formation. The vaccines are used to protect animals (pige,
 CC horses, dogs, cattle, cats or birds) against a wide variety of viral or
 CC bacterial infections
 XX
 SQ Sequence 1698 BP; 618 A; 320 C; 369 G; 391 T; 0 U; 0 Other;
 Query Match 96.1%; Score 1019.2; DB 2; Length 1698;
 Best Local Similarity 99.2%; Pred. No. 1.8e-277;
 Matches 1024; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 30 ATGAAGACACACCATTTATTTGATCTACTACTGACCCATTTATGCTGGGACACCATG 89
 Db 1 ATGAAGACACCATTTATTTGATCTACTACTGACCCATTTATGCTGGGACACCATG 60
 QY 90 AGTGGAAACAACACACCATTTATGCTGGGACACCATGACATGCAATGGAACATTTG 149
 Db 61 AGTGGCAACAACACACCATTTATGCTGGGACACCATGACATGCAATGGAACATTTG 120
 QY 150 GTAAAAACAATACTGATGACCAATTTAGGTGACAAATGCTACTGAATTTAGTTCAGAC 209
 Db 121 GTAAAAACAATACTGATGACCAATTTAGGTGACAAATGCTACTGAATTTAGTTCAGAC 180
 QY 210 ATTTCAATAGGGAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTCACA 269
 Db 181 ATTTCAATAGGGAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTCACA 240
 QY 270 TTAATAGATGCAATGCTAGGAGACCCCACTGTGTGTCTTCCAGTATGAGAAATTTGGAC 329

Db 241 TTAATAGATGCAATGCTAGGAGACCCCACTGCTGATGCTTTCAGTATGAGAAATGGGAC 300
 Qy 330 CTCCTTATAGAAAGAGCAGCGCTTTCAGCAATGCTACCATATGACATCCCTGACTAT 389
 Db 301 CTCCTTATAGAAAGAGCAGCGCTTTCAGCAATGCTACCATATGACATCCCTGACTAT 360
 Qy 390 GCATCGCTCCGCTCCATTTAGTATGCTTCCAGCAATGCTACCATATGACATCCCTGACTAT 449
 Db 361 GCATCGCTCCGCTCCATTTAGTATGCTTCCAGCAATGCTACCATATGACATCCCTGACTAT 420
 Qy 450 ACATGGACAGTGTCTCACTCAAAACGGAAGAGTGGAGCTTCCAAAGAGGAGATTC 509
 Db 421 ACATGGACAGTGTCTCACTCAAAACGGAAGAGTGGAGCTTCCAAAGAGGAGATTC 480
 Qy 510 AGTTCTTTAGCCGACTGAAATGCTTACAAATCTGGAATCTTACCCACATGGAAT 569
 Db 481 AGTTCTTTAGCCGACTGAAATGCTTACAAATCTGGAATCTTACCCACATGGAAT 540
 Qy 570 GTGCAATGCTTAAATTAATAATTTCCAAACCTATACATCTGGGGATTCATCACCG 629
 Db 541 GTGCAATGCTTAAATTAATAATTTCCAAACCTATACATCTGGGGATTCATCACCG 600
 Qy 630 AGCTCAAAACCAACGAGAGAGATTTGATCCAAAGATCAGACGAGTAACAGTCTCA 689
 Db 601 AGCTCAAAACCAACGAGAGAGATTTGATCCAAAGATCAGACGAGTAACAGTCTCA 660
 Qy 690 ACAAAGAGTCAACCAACATAGTCCCTTAATATCGATCTAGACCGTGGTGGGTTAGGGT 749
 Db 661 ACAAAGAGTCAACCAACATAGTCCCTTAATATCGATCTAGACCGTGGTGGGTTAGGGT 720
 Qy 750 CAATCAGCAGGATGAAGATATCTAGCAATCTGGAACCTGAGATATCTTAATGATA 809
 Db 721 CAATCAGCAGGATGAAGATATCTAGCAATCTGGAACCTGAGATATCTTAATGATA 780
 Qy 810 AACAGTATGCAATTTAGTTCACCGCGGATATTTAAATTTGAAAACAGGAGGAAAGC 869
 Db 781 AACAGTATGCAATTTAGTTCACCGCGGATATTTAAATTTGAAAACAGGAGGAAAGC 840
 Qy 870 TCTGTATGATGATCAGATGACACCATATGACATTTGCTGTGCTGATATTAACCAAT 929
 Db 841 TCTGTATGATGATCAGATGACACCATATGACATTTGCTGTGCTGATATTAACCAAT 900
 Qy 930 GGAAGCATCCCCAAGCAACCAATTTCAAAATGGAACAAAGTTACATATGAAATATGC 989
 Db 901 GGAAGCATCCCCAAGCAACCAATTTCAAAATGGAACAAAGTTACATATGAAATATGC 960
 Qy 990 CCCAAGTATATCAGGCAAAACATTTTAAAGCTGGCCATCGGATGAGGAATATACAGAA 1049
 Db 961 CCCAAGTATATCAGGCAAAACATTTTAAAGCTGGCCATCGGATGAGGAATATACAGAA 1020
 Qy 1050 AAGCAATTCAGA 1061
 Db 1021 AAGCAATTCAGA 1032

RESULT 5

ID AAQ29112 standard; DNA; 1762 BP.
 XX AC AAQ29112;
 XX AC AAQ29112;
 DT 25-MAR-2003 (revised)
 DT 24-FEB-1993 (first entry)
 XX XX
 DE EIV HA (A2/Suffolk/89).
 XX Equine influenza virus; EIV; hemagglutinin; HA; A2/Suffolk/89;
 KW expression cassette; NYVAC; ALVAC; recombinant vector; M13;
 KW polymerase chain reaction; PCR; vaccinia virus; i3L promoter;
 KW canarypox virus; Copenhagen vaccine strain; virulence factor;
 KW deletion loci; recipient loci; ss.

OS Synthetic.
 PN WO9215672-A1.
 XX 17-SEP-1992.
 PF 09-MAR-1992; 92WO-US001906.
 XX 07-MAR-1991; 91US-00666056.
 PR 11-JUN-1991; 91US-00713967.
 PR 06-MAR-1992; 92US-00847951.
 XX (VIRO-) VIROGENETICS CORP.
 XX Paoletti E, Perkus ME, Taylor J, Tartaglia J, Norton EK;
 PI Riviere M, De Taine C, Limbach KJ, Johnson GP, Pincus SE, Cox WI;
 PI Francis J, Gettig RR;
 XX WPI; 1992-331718/40.
 DR Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating
 XX against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,
 PT mumps etc.
 PS Disclosure; Fig 25; 456pp; English.
 CC The sequence given encodes the equine influenza virus (EIV) hemagglutinin
 CC (HA) (A2/Suffolk/89). This sequence was used to generate an expression
 CC cassette for the insertion of the EIV HA gene into NYVAC and ALVAC
 CC recombinant vectors. The HA gene sequence was isolated by polymerase
 CC chain reaction from an M13 clone. Some non-conserved base-changes were
 CC observed due to the amplification process. The EIV HA gene was linked to
 CC the i3L promoter and inserted into a vaccinia insertion plasmid deleted
 CC for ORF-8 CGL-KIL. NYVAC is derived from a Copenhagen vaccine strain of
 CC vaccinia virus and ALVAC is derived from a canarypox virus which has been
 CC modified by deletion of non-essential regions of the genome encoding
 CC known or potential virulence factors. The deletion loci of both vectors
 CC were engineered as recipient loci for the insertion of foreign genes. See
 CC also AAQ35501-864. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 1762 BP; 637 A; 328 C; 384 G; 412 T; 0 U; 1 Other;
 Query Match 96.0%; Score 1018.4; DB 2; Length 1762;
 Best Local Similarity 97.5%; Pred. No. 3.1e-277;
 Matches 1034; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
 Qy 1 AGCAAAAGCAGGGGATATTTCTGCAATCATGAAGACAACCATTTATTTGATCTACTGA 60
 Db 1 AGCAAAAGCAGGGGATATTTCTGCAATCATGAAGACAACCATTTATTTGATCTACTGA 60
 Qy 61 CCCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGAAACAACACAGCCACATTATGCTGG 120
 Db 61 CCCATTGGGTCTACAGTCAAAACCCCAACCAAGTGGAAACAACACAGCCACATTATGCTGG 120
 Qy 121 GACACCATGTCAGTAGCAAAATGGAACATTTGGTAAAAACAATACTGTATGACCAAAATTCAGG 180
 Db 121 GACACCATGTCAGTAGCAAAATGGAACATTTGGTAAAAACAATACTGTATGACCAAAATTCAGG 180
 Qy 181 TGACAAATGCTACTGAAATTTAGTTCAGAGCATTTTCAATAGGGAATAATGCAACATTCAT 240
 Db 181 TGACAAATGCTACTGAAATTTAGTTCAGAGCATTTTCAATAGGGAATAATGCAACATTCAT 240
 Qy 241 ATAAAGTTCCTAGATGGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300
 Db 241 ATAGGGTTCCTAGATGGAAGAAATTTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300
 Qy 301 GTGATGCTCTTCCAGTATGAGAAATTTGGACCTCTTTCATAGAAAGAGCAGCGCTTTTCAGCA 360
 Db 301 GTGATGCTCTTCCAGTATGAGAAATTTGGACCTCTTTCATAGAAAGAGCAGCGCTTTTCAGCA 360
 Qy 361 ATTGCTACCATATGATCATCCCTGACTATGATCGCTCGGTTCATTTAGTATGATCTCTCAG 420
 Db 361 ATTGCTACCATATGATCATCCCTGACTATGATCGCTCGGTTCATTTAGTATGATCTCTCAG 420

QY 421 GAACATTAGAAATTCACAGCAGAGGGATTACATGGACAGGTGTCACTCAAAACGGAAGA 480
Db |||||||
QY 421 GAACATTAGAAATTCACAGCAGAGGGATTACATGGACAGGTGTCACTCAAAACGGAAGA 480
Db |||||||
QY 481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTAACAA 540
Db |||||||
QY 541 AATCTGGAATCTTACCCACACATTGATGTGCAATGCTTAACAATAAAATTTTGACA 600
Db |||||||
QY 541 AATCTGGAATCTTACCCACACATTGATGTGCAATGCTTAACAATAAAATTTTGACA 600
Db |||||||
QY 601 AACTATACATCTGGGGATTTCATCACCCGAGCTCAAAACAGCAGACAGAGATTGTGACA 660
Db |||||||
QY 601 AACTATACATCTGGGGATTTCATCACCCGAGCTCAAAACAGCAGACAGAGATTGTGATA 660
Db |||||||
QY 661 TCCAAGAAATCAGGACGAGTTAACAGTCTCAACAAAAGAGAGTCAACAAAGATAGTCCCTA 720
Db |||||||
QY 661 TCCAAGAAATCAGGACGAGTTAACAGTCTCAACAGAGAGAGTCAACAAAGATAGTCCCTA 720
Db |||||||
QY 721 ATATCGGATCAGACCGTGGGTTAGGGTCAATCAGCAGGATAAGCATATAGTACCA 780
Db |||||||
QY 721 ACATCGGATCAGACCGTGGGTTAGGGTCAATCAGCAGGATAAGCATATAGTACCA 780
Db |||||||
QY 781 TTGTAAACCTGGAGATATCTTAATGATAAACAGTAAATGGCAACTTAGTTGCAACCGGG 840
Db |||||||
QY 781 TTGTAAACCTGGAGATATCTTAACGATAAACAGTAAATGGCAACTTAGTTGCAACCGGG 840
Db |||||||
QY 841 GATATTTTAAATGAAACAGGGAAGCTCTGTAATGAGATCAGATGCAACCCATAGACA 900
Db |||||||
QY 841 GATATTTTAAATGAAACAGGGAAGCTCTGTAATGAGATCAGATGCAACCCATAGACA 900
Db |||||||
QY 901 TTTGTGTCTGATGTATTACACCAATGGAAGCATCCCCACGACAAACCATTTTCAA 960
Db |||||||
QY 901 CTTGTGTCTGATGTATTACACCAATGGAAGCATCCCCACGACAAACCATTTTCAA 960
Db |||||||
QY 961 ATGTGAACAAAGTTACATATGGAATGCCCCAAGTATATCAGGCAAAACACITTTAAAGC 1020
Db |||||||
QY 961 ATGTGAACAAAGTTACATATGGAATGCCCCAAGTATATCAGGCAAAACACITTTAAAGC 1020
Db |||||||
QY 1021 TGSCCACTGGATGAGGAATATACCGAAAGCAAAATCAGA 1061
Db |||||||
QY 1021 TGSCCACTGGATGAGGAATATACCGAAAGCAAAATCAGA 1061
Db |||||||

RESULT 6

AAN71067
ID AAN71067 standard; DNA; 1788 BP.
XX
AC AAN71067;
XX
DT 08-MAR-1991 (first entry)
XX
DE Sequence encoding equine influenza virus strain H3N8 (EIV-A2)
DE haemagglutinin protein H3.
XX
KW HA; vaccine; Vaccina; ds.
XX
OS Equine influenza virus.
XX
FH Key Location/Qualifiers
FT CDS 54..1748
FT /*tag= a
FT mat_peptide 102..1082
FT /label= HA 1
FT mat_peptide 1086..1748
FT /*tag= c
FT /label= HA 2
XX
FN WO8607593-A.
XX

PD 31-DEC-1986.
XX
PF 20-JUN-1986; 86WO-US001343.
XX
PR 20-JUN-1985; 85US-00747020.
XX
PA (BIOT-) BIOTECHN RES PARTNE.
XX
PI Dale B, Cordell B;
XX
XX WPI; 1987-007191/01.
DR P-PSDB; AAP70711.
XX
PT Preventing equine influenza virus infection - using recombinant vaccines
PT produced using DNA sequences encoding haemagglutinin and neuraminidase
PT glyco:proteins.
XX
PS Disclosure; Fig 2; 63pp; English.
XX
XX Peptides derived from the haemagglutinin H7 and H3 and neuraminidase N7
CC and N8 genes may be used to derive antigenic peptides useful in
CC vaccination against equine influenza virus infection. Abs raised to the
CC peptides may be used in diagnosis of the infection and construction of
CC probes to mutated forms of the virus
XX
SQ Sequence 1788 BP; 637 A; 340 C; 409 G; 402 T; 0 U; 0 Other;
Query Match 93.1%; Score 987.4; DB 1; Length 1788;
Best Local Similarity 95.7%; Pred. No. 1.8e-268;
Matches 1015; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 1 AGCAAAAGCAGGGATATTTCTGTCAATCATGAAGCAACCACTATTTTGTACTACTGA 60
Db 25 AGCAAAAGCAGGGATATTTCTGTCAATCATGAAGCAACCACTATTTTGTACTACTGA 84
QY 61 CCCATTGGTCTACAGTCAAAACCCCAACCCAGTGGAAACACACAGCCACATTATGTCTG 120
Db 85 CCCATTGGTCTACAGTCAAAACCCCAACCCAGTGGAAACACACAGCCACATTATGTCTG 144
QY 121 GACACATCAGTAGCAAAATGGAACATTTGGTAAAAAACAATTAAGTACCAATTTGAGG 180
Db 145 GACACATCAGTAGCAAAATGGAACATTTGGTAAAAAACAATTAAGTACCAATTTGAGG 204
QY 181 TGACAAATGCTACTGAAATTTAGTTTCAGAGCAATTTCAATAGGAAAAATATGCAACAACTCAT 240
Db 205 TGACAAATGCTACTGAAATTTAGTTTCAGAGCAATTTCAATAGGAAAAATATGCAACAACTCAT 264
QY 241 ATAAAGTTCTAGATGGAAGAAATTTGCAATTAATAGATGCAATGCTAGGAGACCCCACT 300
Db 265 ATAGGGTTCTAGATGGAAGAAATTTGGAACCTCTTTCATAGAAAGACAGCGCTTTTCAGCA 324
QY 301 GTGATGTTCTCCAGTATGAGAAATTTGGGACCTCTTTCATAGAAAGACAGCGCTTTTCAGCA 360
Db 325 GTGATGTTCTCCAGTATGAGAAATTTGGGACCTCTTTCATAGAAAGACAGCGCTTTTCAGCA 384
QY 361 ATTGCTACCCATATGACATCCCTGACTATGCTATGCTCCGGTCCATTTGTAGCATCTCTCAG 420
Db 385 ATTGCTACCCATATGACATCCCTGACTATGCTATGCTCCGGTCCATTTGTGGCATCTTCAG 444
QY 421 GAACATTAGAAATTCACAGCAGAGGGATTACATGGACAGGTGTCACTCAAAACGGAAGA 480
Db 445 GAACATTAGAAATTCACAGCAGAGGGATTACATGGACAGGTGTCACTCAAAACGGAAGA 504
QY 481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTAACAA 540
Db 505 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTAACAA 564
QY 541 AATCTGGAATCTTACCCACACATTGATGTGCAATGCTTAACAATAAAATTTTGACA 600
Db 565 AATCTGGAATCTTACCCACACATTGATGTGCAATGCTTAACAATAAAATTTTGACA 624
QY 601 AACTATACATCTGGGGATTTCATCACCCGAGCTCAAAACAGCAGACAGAGATTGTGACA 660
Db |||||||

Db 625 AACTATACATCTGGGGGATCCATCACCCGAGCACAAACAATGAGCAGACAAAATTTGTATA 684
QY 661 TCCAAAGATCAGGACGAGTAACAGTCTCAACAAAAGAGTCAACAAACGATAGTCCCTA 720
Db 685 TCCAAAGATCAGGACGAGTAACAGTCTCAACAAAAGAGTCAACAAACGATAGTCCCTA 744
QY 721 ATATCGGATCTAGACCGGTAGGAGTCAATCAGGAGGATAGCATATATCTGGACCA 780
Db 745 ACATCGGATCTAGACCGGTAGGAGTCAATCAGGAGGATAGCATATATCTGGACCA 804
QY 781 TTGTAAACCTGGAGATATCTTAATGATAAAGTAAATGGCACTTAGTTGGACCGGG 840
Db 805 TTGTAAACCTGGAGATATCTTAATGATAAAGTAAATGGCACTTAGTTGGACCGGG 864
QY 841 GATATTTTAAATGAAAACAGGAAAAGCTCTGTAATGAGATCAGATGACCCATAGACA 900
Db 865 GATATTTTAAATGCGAACAGGAAAAGCTCTGTAATGAGATCAGATGACCCATAGACA 924
QY 901 TTGTGTCTGAATGTAATTAACCAAAATGGAAGCATCCCAACGACAAACCATTTCAA 960
Db 925 CTGTGTCTCGAGTGTATTACACCAAAATGGAAGCATCCCAACGACAAACCATTTCAA 984
QY 961 ATGTGAACAAATGTAATGTAATTAACCAAAATGGAAGCATCCCAACGACAAACCATTTCAA 1020
Db 985 ATGTGAACAAATGTAATGTAATGTAATTAACCAAAATGGAAGCATCCCAACGACAAACCATTTCAA 1044
QY 1021 TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAAATCAGA 1061
Db 1045 TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAAATCAGA 1085

RESULT 7

AAQ04597

ID AAQ04597 standard; DNA; 1797 BP.

XX AC AAQ04597;

XX 25-MAR-2003 (revised)

DT 02-OCT-1990 (first entry)

XX XX Equine hemagglutinin H3 (EIV-A2).

XX XX Recombinant vaccines; equine influenza virus; haemagglutinin; H3;

KW neuraminidase; N8; ss.

XX OS Equine influenza virus.

XX FH Key Location/Qualifiers

FT CDS 54..1748

FT /*tag= a

FT /product= "EIV-A2 haemagglutinin H3"

FT misc_RNA 102..1182

FT /*tag= b

FT /product= "N-terminal HA1 50kD portion"

FT misc_RNA 1186..1748

FT /*tag= c

FT /product= "C-terminal HA2 27kD portion"

XX XX US4920213-A.

XX 24-APR-1990.

XX 21-JUL-1986; 86US-00888250.

XX 20-JUN-1985; 85US-00747020.

XX (BIOT-) BIOTECH RES PARTNERS LTD.

XX Dale B, Cordell B;

XX WPI; 1990-163647/21.

XX P-PSDB; AAR04943.

PT Recombinant vaccines against equine influenza virus - produced using DNA
PT sequences encoding haemagglutinin and neuraminidase glyco-protein(s).
XX Disclosure; Page ?; 27pp; English.

CC There are nine neuraminidase (NA) subtypes and twelve haemagglutinin (HA)
CC subtypes. The strain carrying H3N8 glycoproteins is designated equine
CC influenza virus (EIV)-A2. The cDNA sequences encoding these will be
CC useful in the construction of diagnostic probes for the disease and of
CC probes for obtaining new cDNAs of the mutated form of the virus.
CC Recombinant vaccines are produced. See also AAQ04596-Q04599. (Updated on
CC 25-MAR-2003 to correct PA field.)

SQ Sequence 1797 BP; 639 A; 341 C; 413 G; 404 T; 0 U; 0 Other;

Query Match 93.1%; Score 987.4; DB 2; Length 1797;

Best Local Similarity 95.7%; Pred. No. 1.8e-268;

Matches 1015; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAGACAAACCATTTATTTGATACTACTGA 60
Db 25 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAGACAAACCATTTATTTGATACTACTGA 84
QY 61 CCCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGCAACACACACACACTATGTCTGG 120
Db 85 CCCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGCAACACACACACACTATGTCTGG 144
QY 121 GACACCATGCAAGTAGCAAAATGGAACATTTGTAATAAACAATACTGATGACCAATTTGAGG 180
Db 145 GACACCATGCAAGTAGCAAAATGGAACATTTGTAATAAACAATACTGATGACCAATTTGAGG 204
QY 181 TGACAAATGCTACTGAAATTTAGTTTCTGAGACACTTCAATAGGAAAATATGCAACCACTAT 240
Db 205 TGACAAATGCTACTGAAATTTAGTTTCTGAGACACTTCAATAGGAAAATATGCAACCACTAT 264
QY 241 ATAAAGTTCTAGATGGAAGAAATTTGCACATTAATAGATGCAATCTAGGAGACCCCACT 300
Db 265 ATAGGGTTCTAGATGGAAGAAATTTGCACATTAATAGATGCAATCTAGGAGATCCCACT 324
QY 301 GTGATGCTTCCAGTATGAGAAATTTGGACCTCTTCTATAGAAAGAGCAGCGCTTTTCAGCA 360
Db 325 GTGATGCTTTCAGTATGAGAAATTTGGACCTCTTCTATAGAAAGAGCAGCGCTTTTCAGCA 384
QY 361 ATTGCTACCATATGACATCCCTGACATATGATGCTGCTCCGCTCCATTTAGTACCTCTAG 420
Db 385 ATTGCTACCATATGACATCCCTGACATATGATGCTGCTCCGCTCCATTTAGTACCTCTAG 444
QY 421 GAACATTAGAAATTCACAGCAGAGGATTCACATGGACAGCGTGTCACTCAAAACCGAAGAA 480
Db 445 GAACATTAGAAATTCACAGCAGAGGATTCACATGGACAGCGTGTCACTCAAAACCGAAGAA 504
QY 481 GTGAGCCTCCAAAGGGGATCAGCGGATAGTTTCTTTAGCCGACTGAATTTGGCTAAACAA 540
Db 505 GTGAGCCTCCAAAGGGGATCAGCGGATAGTTTCTTTAGCCGACTGAATTTGGCTAAACAA 564
QY 541 AATCTGAAACTCTTACCCACATTTGAAATGTAACAATGCTTAAATAAATAATTTTCACA 600
Db 565 AATCTGAAACTCTTACCCACATTTGAAATGTAACAATGCTTAAATAAATAATTTTCACA 624
QY 601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGTACA 660
Db 625 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAACAGCAGACAGAAATTTGTACA 684
QY 661 TCCAAGATCAGGACGAGTAAAGTCTCAACAAAAAGAGTCAACAAACATAGTCCCTA 720
Db 685 TCCAAGATCAGGACGAGTAAAGTCTCAACAAAAAGAGTCAACAAACATAGTCCCTA 744
QY 721 ATATCGGATCTAGACCGGTAGGAGTCAATCAGGAGGATAGCATATATCTGGACCA 780
Db 745 ACATCGGATCTAGACCGGTAGGAGTCAATCAGGAGGATAGCATATATCTGGACCA 804
QY 781 TTGTAAACCTGGAGATATCTTAATGATAAAGTAAATGGCACTTAGTTGGACCGGG 840

Db 805 TTGTGAACCTGGAGATATCTTAATGATAACAGTAATGGCAACTTAGTTGCACCGGG 864
Qy 841 GATATTTTAAATTTGAAACAGGGAAGCTCTGTAATGAGATCAGATGCACCCATAGACA 900
Db 865 GATATTTTAAATTTGCGAACAGGGAAGCTCTGTAATGAGATCAGATGCACCCATAGACA 924
Qy 901 TTTGTGTGCTGAATGTATTACCAAAATGGAAGCATCCCCAACGACAAACCAATTTCAAA 960
Db 925 CTTGTGTGCTCGAGTGTATTACCAAAATGGAAGCATCCCCAACGACAAACCAATTTCAAA 984
Qy 961 ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACATTTAAAGC 1020
Db 985 ATGTGAACAAAGTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACATTTAAAGC 1044
Qy 1021 TGGCCACTGGGATGAGGAATATACCGAAGCAAAATCAGA 1061
Db 1045 TGGCCACTGGGATGAGGAATGTACCGAAGCAAAATCAGA 1085

RESULT 8

ID AAZ30211 standard; DNA; 1698 BP.

AC AAZ30211;

XX 11-FEB-2000 (first entry)

XX Sequence of the haemagglutinin (HA) gene of EIV strain Newmarket 2/93.

XX Haemagglutinin gene; EIV, strain Newmarket 2/93; DNA vaccine; horse;
KW acrylic acid polymer; methacrylic acid polymer; copolymer;
KW maleic anhydride; alkenyl derivative; animal vaccine; viral infection;
KW bacterial infection; SS.

XX Equine influenza virus.

XX FR2776928-A1.

XX 08-OCT-1999.

XX 03-APR-1998; 98FR-00004409.

XX 03-APR-1998; 98FR-00004409.

XX (MERI-) MERIAL SAS.

XX Audonnet JCF, Minke JM;

XX WPI; 1999-593389/51.

XX Vaccine containing naked DNA and acrylic acid polymer or maleic anhydride
PT copolymer, for protection against viral or bacterial diseases in animals.

XX Example 8; Fig 1; 34pp; French.

XX The present sequence represents the haemagglutinin gene of Equine
CC influenza virus (EIV) strain Newmarket 2/93. The sequence was used to
CC prepare a DNA vaccine for horses, representative of the DNA vaccines of
CC the invention. The specification describes a DNA vaccine that comprises
CC naked DNA encoding an antigenic polypeptide, and at least one adjuvant
CC that is an acrylic or methacrylic acid polymer or a copolymer of maleic
CC anhydride with an alkenyl derivative. The vaccines are simple and easy to
CC prepare (simply by mixing components) and they do not involve any strong
CC interactions between DNA and other components that are likely to cause
CC complex formation. The vaccines are used to protect animals (pigs,
CC horses, dogs, cattle, cats or birds) against a wide variety of viral or
CC bacterial infections

XX Sequence 1698 BP; 619 A; 312 C; 372 G; 395 T; 0 U; 0 Other;

Query Match 92.78; Score 984; DB 2; Length 1698;

Best Local Similarity 97.14; Pred. No. 1.6e-267;

Matches 1002; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 30 ATGAAGACCAACCATTTATTTTGATCTACTGACCCATTGGTCTTACAGTCAAAACCCCAACC 89
Db 1 ATGAAGACCAACCATTTATTTTGATCTACTGACCCATTGGTCTTACAGTCAAAACCCCAACC 60
Qy 90 AGTGGAAAACAACAAGCCCATTTATGTCTGGGACACCATGTCAGTAGCAAAATGGAAACATTG 149
Db 61 AGTGGCAACAACAAGCCCATTTATGTCTGGGACACCATGTCAGTAGCAAAATGGAAACATTG 120
Qy 150 GTAAAAACAATACTGATGACCAAAATGAGGTGACAAATGCTACTGAAATAGTTTCAGAGC 209
Db 121 GTAAAAACAATACTGATGACCAAAATGAGGTGACAAATGCTACTGAAATAGTTTCAGAGC 180
Qy 210 ATTTCAATAGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTCACACA 269
Db 181 ATTTCAATAGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTCACACA 240
Qy 270 TTAATAGATGCAATGCTAGGAGACCCCACTGTGTGATGTCTTCCAGTATGAGAATTTGGGAC 329
Db 241 TTAATAGATGCAATGCTAGGAGACCCCACTGTGTGATGTCTTCCAGTATGAGAATTTGGGAC 300
Qy 330 CTCTTCATAGAAAAGAGCAGCGCTTTTCAGCAATTTGCTACCCATATGACATGCCCTGACTAT 389
Db 301 CTCTTCATAGAAAAGAGCAGCGCTTTTCAGCAATTTGCTACCCATATGACATGCCCTGACTAT 360
Qy 390 GCATCGCTCCGGTCCATTGTCATCCTCAGGAACATTAGAAATTCACAGCAGAGGATTC 449
Db 361 GCATCGCTCCGGTCCATTGTCATCCTCAGGAACATTAGAAATTCACAGCAGAGGATTC 420
Qy 450 ACATGAGACAGGTGTCTCACTCAAAACGGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
Db 421 ACATGAGACAGGTGTCTCACTCAAAACGGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 480
Qy 510 AGTTTCTTTAGCCGACTGAATTTGGCTAAACAAAATCTGGAACCTTTACCCCAATTTGAAT 569
Db 481 AGTTTCTTTAGCCGACTGAATTTGGCTAAACAAAATCTGGAACCTTTACCCCAATTTGAAT 540
Qy 570 GTGACAAATGCCTAAACAATAAATAATTTTCGACAAACTATACATCTGGGGGATTCATACCCCG 629
Db 541 GTGACAAATGCCTAAACAATAAATAATTTTCGATAAACTATACATCTGGGGGATTCATACCCCG 600
Qy 630 AGCTCAAAACAACAGCAGACAGAAATTTGTATCATCCAAAGAAATCAGGACGAGTAACAGTCTCA 689
Db 601 AGCTCAAAACAACAGCAGACAGAAATTTGTATATCCAAAGAAATCAGGACGAGTAACAGTCTCA 660
Qy 690 ACAAAAGAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGGTTCAGGGGT 749
Db 661 ACAAAAGAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGGTTCAGGGGT 720
Qy 750 CAATCAGGACGAGTAAAGCATATATCTGGACCATTTGTAACACCTGGAGATATCCTTAATGATA 809
Db 721 CAATCAGGACGAGTAAAGCATATATCTGGACCATTTGTAACACCTGGAGATATCCTTAATGATA 780
Qy 810 AACAGTAAATGGCAACTTAGTTGCAACCGCGGGATATTTTAAATTTGAAAAACAGGAAAAAGC 869
Db 781 AACAGTAAATGGCAACTTAGTTGCAACCGCGGGATATTTTAAATTTGAAAAACAGGAAAAAGC 840
Qy 870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGTAATGTAATACACCAAT 929
Db 841 TCTGTAATGAGATCAGATGCACCTATAGACATTTGTGTCTGTAATGTAATACACCAAT 900
Qy 930 GGAAGCATCCCCAACGACAAACCATTTTCAAAATGTGAACAAAGTTACATATGGAATATGC 989
Db 901 GGAAGCATCCCCAACGACAAACCATTTTCAAAATGTGAACAAATTTACATATGGAATATGC 960
Qy 990 CCCAAGTATATCGGCAAAACACTTTTAAAGCTGGCCACTGGGATGAGGATATACAGAA 1049
Db 961 CCCAAGTATATCGGCAAAACACTTTTAAAGCTGGCCACTGGGATGAGGATATACAGAA 1020
Qy 1050 AAGCAAAATCAGA 1061
Db 1021 AAGCAAAATCAGA 1032


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RESULT 9
AAZ47007
ID AAZ47007 standard; DNA; 1698 BP.
XX
AC
XX
AC
XX
DT 29-FEB-2000 (first entry)
XX
DE Equine influenza virus strain Newmarket 2/93 HA gene.
XX
KW Antibacterial; antiviral; primer; RT-PCR; amplification; haemagglutinin;
KW recombinant; vaccine; viral vector; pathogen; adjuvant; methacrylic acid;
KW maleic anhydride; alkenyl derivative; animal; herpes virus; tetanus;
KW influenza virus; feline leukemia; canine distemper; ss.
XX
OS Equine influenza virus.
XX
XX WO9944633-A1.
XX
XX 10-SEP-1999.
XX
XX 01-MAR-1999; 99WO-FR000453.
XX
XX 03-MAR-1998; 98FR-00002800.
XX
XX (MERI-) MERIAL.
XX
XX Audonnet JF, Minke JM;
XX
XX WPI; 2000-022918/02.
XX
XX Live recombinant vaccine comprising viral vector and polymeric adjuvant,
XX particularly directed against animal herpes and influenza viruses.
XX
XX Example 5; Fig 1; 41pp; French.
XX
XX This sequence represents the haemagglutinin (HA) gene from the equine
XX influenza virus strain Newmarket 2/93. The gene was amplified and the
XX product was used to generate a live recombinant vaccine which comprises:
XX (1) a viral vector including, and expressing in vivo, a heterologous
XX nucleotide sequence particularly a gene from a pathogen; and (2) at least
XX one adjuvant, i.e. a (meth)acrylic acid polymer or a copolymer of maleic
XX anhydride and alkenyl derivatives. The vaccines are used particularly to
XX protect against animal herpes or influenza viruses, but also feline
XX leukemia, tetanus and canine distemper
XX
XX Sequence 1698 BP; 619 A; 312 C; 372 G; 395 T; 0 U; 0 Other;
Query Match 92.7%; Score 984; DB 3; Length 1698;
Best Local Similarity 97.1%; Pred. No. 1.6e-267;
Matches 1002; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 30 ATGAAGACAAACCAATTTTGTATCTACTACTGACCCATTGGGTCTACAGTCAAAACCCCAACC 89
DB 1 ATGAAGACAAACCAATTTTGTATCTACTACTGACCCATTGGGTCTACAGTCAAAACCCCAACC 60
QY 90 AGTGGAAACACACAGGCCACCAATTTGTCTGGGACACCATGCTAGCAATGGAACATTTG 149
DB 61 AGTGGCAACACACAGGCCACCAATTTGTCTGGGACACCATGCTAGCAATGGAACATTTG 120
QY 150 GTAAAAACAATACTGTATGACCAAAATTTGAGGTGACAAATGCTACTGAATTTAGTTCAGAGC 209
DB 121 GTAAAAACAATACTGTATGACCAAAATTTGAGGTGACAAATGCTACTGAATTTAGTTCAGAGC 180
QY 210 ATTTCAATAGGAAAAATATGACAACTCATATAAAGTTCTCAGATGGAAGAAATTCACAA 269
DB 181 ATTTCAATAGGAAAAATATGACAACTCATATAAAGTTCTCAGATGGAAGAAATTCACAA 240
QY 270 TTAATAGATGCAATGTAGAGAGACCCCACTGTGTCTTCCAGTATGAGAAATTTGGGAC 329
DB 241 TTAATAGATGCAATGTAGAGAGACCCCACTGTGTGTGATGATTTTCAGTATGAGAAATTTGGGAC 300

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QY 330 CTCTTCATAGAAAGACGACGCGCTTTTCAGCAATTTGCTACCATATGACATCCCTGACTAT 389
DB 301 CTCTTCATAGAAAGACGACGCGCTTTTCAGCAATTTGCTACCATATGACATCCCTGACTAT 360
QY 390 GCATCGCTCCGGTCCATTTGTAGCATCTCTCAGGAACATTAGAAATTTACAGCAGAGGGATTC 449
DB 361 GCATCGCTCCGGTCCATTTGTAGCATCTCTCAGGAACATTAGAAATTTACAGCAGAGGGATTC 420
QY 450 ACATGGACAGGTGTCTCAAAACGGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
DB 421 ACATGGACAGGTGTCTCAAAACGGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 480
QY 510 AGTTTCTTTAGCCGACTGAATTTGGCTAAACAAATCTGAAACTCTTACCCACACATTCGAAT 569
DB 481 AGTTTCTTTAGCCGACTGAATTTGGCTAAACAAATCTGAAACTCTTACCCACATTCGAAT 540
QY 570 GTGCAATGCTTAACAAATAAAAAATTTGCAAACTATACATCTCTGGGGATTTCAACCCG 629
DB 541 GTGCAATGCTTAACAAATAAAAAATTTGCAAACTATACATCTCTGGGGATTTCAACCCG 600
QY 630 AGCTCAAAACCAACAGCAGACAGAAATTTGTACATCAAGAAATCAGACAGATTAACAGTCTCA 689
DB 601 AGCTCAAAACCAAGAGCAGACAAATAATATATATCCAAAGAAATCAGACAGATTAACAGTCTCA 660
QY 690 ACAAAGAAAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGGTAGGGGT 749
DB 661 ACAGAAAGAAAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGGCGGTGGGTAGGGGT 720
QY 750 CAATCAGGAGGATAAGCATATATCTGGACCAATTTGTAACCTGGAGATATCTCTAATGATA 809
DB 721 CAATCAGGAGGATAAGCATATATCTGGACCAATTTGTAACCTGGAGATATCTCTAATGATA 780
QY 810 AACAGTAATGGCAACTTAGTTGCAACCGCGGGATATTTAAATTTGAAAACAGGAAAAGC 869
DB 781 AACAGTAATGGCAACTTAGTTGCAACCGCGGGATATTTAAATTTGAAAACAGGAAAAGC 840
QY 870 TCTGTAATGAGATCAGATGACCCATAGACATTTGTGTCTCAATGTATTACACCAAT 929
DB 841 TCTGTAATGAGATCAGATGACCCATAGACATTTGTGTCTCAATGTATTACACCAAT 900
QY 930 GGAAGCATCCCCAACGACAAACCAATTTCAAAATGTGAACAAAGTTACATATGAAAATGC 989
DB 901 GGAAGCATCCCCAACGACAAACCAATTTCAAAATGTGAACAAATTTACATATGAAAATGC 960
QY 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1049
DB 961 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACAGAA 1020
QY 1050 AAGCAAAATCAGA 1061
DB 1021 AAGCAAAATCAGA 1032

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RESULT 10
AAQ29111

ID AAQ29111 standard; DNA; 1762 BP.

XX AAQ29111;

XX AC
XX 25-MAR-2003 (revised)
DT 24-FEB-1993 (first entry)

XX EIV HA (Al/Fontainbleau/79).

XX Equine influenza virus; EIV; haemagglutinin; HA; Al/Fontainbleau/79;
KW expression cassette; NYVAC; ALVAC; recombinant vector;
KW polymerase chain reaction; PCR; vaccinia virus; H6 promoter;
KW canarypox virus; Copenhagen vaccine strain; virulence factor;
KW deletion loci; recipient loci; ss.

XX Synthetic.

XX OS
XX WO9215672-Al.

PN

XX 17-SBP-1992. 92US-0001906.
 XX 09-MAR-1992; 92US-0001906.
 XX 07-MAR-1991; 91US-0066056.
 PR 11-JUN-1991; 91US-00713967.
 PR 06-MAR-1992; 92US-00847951.
 XX (VIRO-) VIROGENETICS CORP.
 XX Paolletti E, Perkus ME, Taylor J, Tartaglia J, Norton EK;
 PI Riviere M, De Taisne C, Limbach KJ, Johnson GP, Pincus SE, Cox WI;
 PI Francis J, Gettig RR;
 XX WPI; 1992-331718/40.
 XX Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating
 PT against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,
 PT mumps etc.
 XX Disclosure; Fig 24; 456pp; English.
 XX The sequence given encodes the equine influenza virus (EIV) haemagglutinin
 CC (HA) (Al/Fontainebleau/79). This sequence was used to generate an
 CC expression cassette for the insertion of the EIV HA gene into NYVAC and
 CC ALVAC recombinant vectors. The HA gene sequence was isolated from an EIV
 CC cDNA library and was amplified by polymerase chain reaction. The HA gene
 CC sequence was fragmented and then reconstituted aligned with the vaccinia
 CC virus H6 promoter. NYVAC is derived from a Copenhagen vaccine strain of
 CC vaccinia virus. ALVAC is derived from a canarypox virus which has been
 CC modified by deletion of non-essential regions of the genome encoding
 CC known or potential virulence factors. The deletion loci of both vectors
 CC were engineered as recipient loci for the insertion of foreign genes. See
 CC also AAQ35501-864. (Updated on 25-MAR-2003 to correct PN field.)
 XX .
 SQ Sequence 1762 BP; 626 A; 331 C; 395 G; 410 T; 0 U; 0 Other;
 Query Match 92.0%; Score 976.2; DB 2; Length 1762;
 Best Local Similarity 95.0%; Pred. No. 2.7e-265;
 Matches 1008; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
 QY 1 AGCAAAAGCAGGGGATATTTCTGCAATCATGAGCAACCAATATTTGATACACTGA 60
 DB 1 AGCAAAAGCAGGGGATATTTCTGCAATCATGAGCAACCAATATTTGATACACTGA 60
 QY 61 CCCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGAAACACACACACATATGCTGG 120
 DB 61 CCCATTGGGTCTACAGTCAAAACCCCAACCCAGTGGCAACACACACACATATGCTGG 120
 QY 121 GACACCATGCGTAGCAAAATGGAAACATTTGGTAAACCAATACTGATGACCAATTTGAGG 180
 DB 121 GACACCATGCGTAGCAAAATGGAAACATTTGGTAAACCAATACTGACGACCAATTTGAGG 180
 QY 181 TGCAAAATGCTACTGAATAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 240
 DB 181 TGCAAAATGCTACTGAATAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 240
 QY 241 ATAAAGTCTCTAGATGGAGAAATGGCAATATGATGCAATGATGCAATGATGCAATGATG 300
 DB 241 ATAGGGTCTCTAGATGGAGAAATGGCAATATGATGCAATGATGCAATGATGCAATGATG 300
 QY 301 GTGATGCTTCCAGTATGAGAAATGGGACCTCTTTCATAGAAAGACAGCGCTTTTCAGCA 360
 DB 301 GTGATGCTTCCAGTATGAGAAATGGGACCTCTTTCATAGAAAGACAGCGCTTTTCAGCA 360
 QY 361 ATTGCTACCATATGACATCCCTGACTATGATGATGATGATGATGATGATGATGATGATG 420
 DB 361 ATTGCTACCATATGACATCCCTGACTATGATGATGATGATGATGATGATGATGATGATG 420
 QY 421 GAACATTTAGAAATTCACAGCAGGGGATTCACATGAGAGGTGTCACATCAAAACGGAAGA 480
 DB 421 GAACATTTAGAAATTCACAGCAGGGGATTCACATGAGAGGTGTCACATCAAAACGGAAGA 480

QY 481 GTGGAGCCTCGAAAAAGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTCGCTAAACAA 540
 DB 481 GTGGAGCCTCGAAAAAGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTCGCTAAACAG 540
 QY 541 AATCTGGAAAATCTTTACCCCAATTTGAATGTGCAATGCTTAACTAAATAATTTTCGACA 600
 DB 541 AATCTGGAAAATCTTTACCCCAATTTGAATGTGCAATGCTTAACTAAATAATTTTCGATA 600
 QY 601 AACTATACATCTGGGGGATTCATCACCAGAGTCAATCACCAGAGCAAACTAGGAGCAAAAATTTGATG 660
 DB 601 AACTATACATCTGGGGGATTCATCACCAGAGTCAATCACCAGAGCAAACTAGGAGCAAAAATTTGATG 660
 QY 661 TCCAAGAATCAGGACGAGTAAACAGTCTCAACAAAAAGAAAGTCAACAAACGATAGTCCCTTA 720
 DB 661 TCCAAGAATCAGGACGAGTAAACAGTCTCAACAAAAAGAAAGTCAACAAACGATAGTCCCTTA 720
 QY 721 ATATCGGATCTAGACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
 DB 721 ATATCGGATCTAGACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
 QY 781 TTGTAAAAACCTCGAGATATCTTAATGATAAAACAGTAATGGCAACTTAGTTGCACCGCGG 840
 DB 781 TTGTAAAAACCTCGAGATATCTTAATGATAAAACAGTAATGGCAACTTAGTTGCACCGCGG 840
 QY 841 GATATTTTAAATTTGAAAAACAGGAAAAAGCTCTGTATGAGATCAGATGACCCCATAGACA 900
 DB 841 GATATTTTAAATTTGAAAAACAGGAAAAAGCTCTGTATGAGATCAGATGACCCCATAGACA 900
 QY 901 TTTGTGTCTGAATGTATACCAAAATGGAAGCATCCCAACGACCAAAACCATTTTCAA 960
 DB 901 TTTGTGTCTGAATGTATACCAAAATGGAAGCATCCCAACGACCAAAACCATTTTCAA 960
 QY 961 ATGTGAAACAAAGTTACATATGAAAAATGCCCAAGTATATCAGGCAAAACACTTTTAAAGC 1020
 DB 961 ATGTGAAACAAAGTTACATATGAAAAATGCCCAAGTATATCAGGCAAAACACTTTTAAAGC 1020
 QY 1021 TGGCCACTGGGATGAGGAATATACCAAGAAAAAGCAAAATCAGA 1061
 DB 1021 TGGCCACTGGGATGAGGAATATACCAAGAAAAAGCAAAATCAGA 1061
 RESULT 11
 AAV49391
 ID AAV49391 standard; DNA; 1698 BP.
 XX
 AC AAV49391;
 XX
 DT 28-OCT-1998 (first entry)
 XX
 DE EIV Fontainebleau strain haemagglutinin gene.
 XX
 KW Multivalent vaccine; horse; pathogen; respiratory disease; EHV; EIV;
 KW Clostridium tetani; Borrelia burgdorferi; equine influenza virus; EEEV;
 KW Eastern equine encephalomyelitis virus; equine herpesvirus; WEEV; VEEV;
 KW Western equine encephalomyelitis virus; digestive disease; rabies virus;
 KW Venezuelan equine encephalomyelitis virus; vector; primer; PCR;
 KW amplification; haemagglutinin; ss.
 XX
 OS Equine influenza virus.
 XX
 FH Key Location/Qualifiers
 FT 1. .1698
 FT CDS /tag= a
 FT /product= "haemagglutinin protein"
 XX
 PR 23-JAN-1998.
 XX 19-JUL-1996; 96PR-00009400.
 XX 19-JUL-1996; 96PR-00009400.

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XX PA (INMR ) RHONE MERIEUX SA.
XX PI Audonnet JCF, Bouchardon A, Riviere MEA;
XX DR WPI; 1998-112826/11.
XX DR P-PSDB; AAW44946.
XX PT Multi-valent polynucleotide vaccines against equine pathogens - consist
XX PT of at least 3 plasmids able to express protective antigens from specified
XX PT viruses.
XX PS Example 14; Fig 8; 49pp; French.
XX CC The invention relates to a multivalent vaccine for protecting horses
XX CC against several pathogens, especially pathogens associated with
XX CC respiratory and digestive diseases. The pathogens are especially selected
XX CC from equine herpesvirus (EHV), equine influenza virus (EIV), Clostridium
XX CC tetani, Borrelia burgdorferi, Eastern, Western or Venezuelan equine
XX CC encephalomyelitis viruses (EEV, WEEV and VEEV, respectively) and rabies
XX CC virus. The vaccines are preferably composed of polynucleotide sequences
XX CC encoding 3 antigens, all as part of vectors. This sequence represents the
XX CC coding region of the EIV Fontainebleau strain haemagglutinin gene. The
XX CC sequence was subcloned into the plasmid pVR1012 to generate plasmid
XX CC pAB099 for use in the vaccine
XX SQ Sequence 1698 BP; 604 A; 319 C; 384 G; 391 T; 0 U; 0 Other;

Query Match      89.3%; Score 947.2; DB 2; Length 1698;
Best Local Similarity 94.9%; Pred. No. 4.2e-257;
Matches 979; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 30 ATGAAGACACCACTATTTTGTACTACTGACCCATTTGGTCTACAGTCAAAACCCNACC 89
DB 1 ATGAAGACACCACTATTTTGTACTACTGACCCATTTGGTCTACAGTCAAAACCCNACC 60

QY 90 AGTGGAAACAACACAGCAGCACATTTATGTCGGGACACCATGAGTAGCAAAATGGAACATTG 149
DB 61 AGTGGCAACAACACAGCAGCACATTTATGTCGGGACACCATGAGTAGCAAAATGGAACATTG 120

QY 150 GTAAAAACAATACTGATGATGACCAAAATTTGAGGTGACAAATGCTACTGAATTTAGTTCAGAGC 209
DB 121 GTAAAAACAATACTGACGACCAAAATTTGAGGTGACAAATGCTACTGAATTTAGTTCAGAGC 180

QY 210 ATTTCATAGGAAATATGCAACAACTCATATAAGTTCTAGATGCAAGAAATTTGCACA 269
DB 181 ACTTCAATAGGAAATATGCAACAACTCATATAAGTTCTAGATGCAAGAAATTTGCACA 240

QY 270 TTAATAGATGAATGCTAGGAGACCCCTGCTGATGCTTCCAGTATGAGAATTTGGAC 329
DB 241 TTAATAGATGAATGCTAGGAGATCCCTGCTGATGCTTCCAGTATGAGAATTTGGAC 300

QY 330 CTCTTCATAGAAAGACAGCGCTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 389
DB 301 CTCTTCATAGAAAGACAGCGCTTTTCAGCAATTTGCTACCCATATGACATCCCTGACTAT 360

QY 390 GCATCGCTCCGTCCTATTTAGTCATCTCAGGAACATTAGAAATTCACAGAGGATTC 449
DB 361 GCATCGCTCCGTCCTATTTAGTCATCTCAGGAACATTAGAAATTCACAGAGGATTC 420

QY 450 ACATGGACAGGTGTCACCTCAAAACGGAAGATGGAGCCTGCAAAAGGGGATCAGCCGAT 509
DB 421 ACATGGACAGGTGTCACCTCAAAACGGAAGATGGAGCCTGCAAAAGGGGATCAGCCGAT 480

QY 510 AGTTTCCTTTAGCCGACTGAATTTGGCTAAACAAATCTGGAACCTTTACCCCAACATTGAAT 569
DB 481 AGTTTCCTTTAGCCGACTGAATTTGGCTAAACAAATCTGGAACCTTTACCCCAACATTGAAT 540

QY 570 GTGACAAATGCTTAACAATAAAATTTTCGACAAACTATATATCTGGGGGATTCATCACCOC 629
DB 541 GTAACAAATGCTTAACAATAAAATTTTCGACAAACTATATATCTGGGGGATTCATCACCOC 600

QY 630 AGCTCAAAACCAACAGCAGCAGACAGAATTTGTATATCCAGAATCAGGACGAGTAAACAGTCTCA 699
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Db 601 AGCACAAACAATGAGCAGACAAAATTTGTATGTCCTCAAGAATTTAGGCGGAGTAAACAGTCTCA 660
QY 690 ACAAAAAGAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGTGGTGGGT 749
Db 661 ACAAAAAGAGTCAACAAACGATAGTCCCTTAATATCGGATCTAGACCGGCGGT 720
QY 750 CAATCAGGAGGAGTAAAGCATATATCTGACCATTTGTAACCTGAGATATCTTAATGATA 809
Db 721 CAATCAGGAGGAGTAAAGCATATATCTGACCATTTGTAACCTGAGATATCTTAATGATA 780
QY 810 AACAGTAATGGCAACTTAGTTGACCCCGGGGATATTTTAAATTTGAAAAACAGGAAAGC 869
Db 781 AACAGTAATGGCAACTTAGTTGACCCCGGGGATATTTTAAATTTGAAAAACAGGAAAGC 840
QY 870 TCTGTAATGAGATCAGATGACCCATGATAGATTTGTGTCTGTAATGTTATACACCAAT 929
Db 841 TCTTAAATGAGATCAGATGACCCATGATAGATTTGTGTCTGTAATGTTATACACCAAT 900
QY 930 GGAAGCATCCCCAACACAAACCATTTTCAAAATGTGAACAAAGTTACATATGAAATGC 989
Db 901 GGAAGCATCCCCAACACAAACCATTTTCAAAATGTGAACAAAGTTACATATGAAATGC 960
QY 990 CCCAAGTATATCAGGCAAAACACTTTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA 1049
Db 961 CCCAAGTATATCAGGCAAAACACTTTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA 1020
QY 1050 AAGCAAAATCAGA 1061
Db 1021 AAGCAAAATCAGA 1032

RESULT 12
AAQ72855
ID AAQ72855 standard; cDNA; 1777 BP.
XX AC AAQ72855;
XX AC AAQ72855;
DT 25-MAR-2003 (revised)
DT 23-JUN-1995 (first entry)
XX Full length H3N2 influenza A virus, strain A2/Aichi/2/68 HA gene.
KW Conserved peptide; stem region; hemagglutinin; HA; H1N1; H2N2; PCR;
KW subtype; human; influenza A virus; immunogenic artificial peptide;
KW antigen; vaccine; infection; polymerase chain reaction; primer; amplify;
KW C179; region A; region B; ds.
XX Influenza A virus.
XX Key Location/Qualifiers
FH CDS 36..1737
FT /*tag= a
FT /product= "Full length HA from H3N2 subtype"
FT sig_peptide 37..84
FT /*tag= b
FT misc_feature 85..246
FT /product= c
FT /*tag= c
FT misc_feature 247..903
FT /product= "Stem region of N-terminal domain"
FT /*tag= d
FT misc_feature 904..1734
FT /product= "Globular head domain"
FT /*tag= e
FT misc_feature 904..1734
FT /product= "Stem region of C-terminal domain"
XX XX
PN BP621339-A2.
XX XX
PD 26-OCT-1994.
XX XX
PF 20-APR-1994; 94BP-00302819.
XX XX
PR 20-APR-1993; 93JP-00115216.
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PR 16-MAR-1994; 94JP-00070194.
XX (TAKI) TAKARA SHUZO CO LTD.
PA
XX Okuno Y, Isegawa Y, Sasao F, Ueda S;
XX WPI; 1994-325949/41.
XX P-PSDB; AAR63590.
DR
XX Human influenza-A virus haemagglutinin polypeptide(s) - useful in
PT influenza-A vaccine composition.
PT
XX Example 2; Page 54-58; 68pp; English.
XX
CC This sequence was amplified using the primer sequences given in AAQ72852-
CC 54 and represents a cDNA which encodes the full length hemagglutinin (HA)
CC gene of the H3N2 subtype of human influenza A virus, strain
CC A2/Aichi/2/68. The full length protein encoded by this amplified cDNA
CC contains two conserved regions, the A' region, TGMN and the B region,
CC QINGKLN(L/V)IEK. These regions are close to each other in the stem of
CC the HA molecule and they represent epitopes which are recognised by the
CC antibody C179. C179 binds to the stem region of the HA molecule and thus
CC inhibits the membrane fusion action of the HA molecule and neutralises
CC the virus. Polypeptide molecules which contain the conserved peptide
CC regions, A and B, esp. HA molecules lacking the globular head region (see
CC also AAQ72807), are antigenically equivalent to the stem region of the HA
CC molecule of influenza A virus. These artificial peptides may be used as
CC vaccines for prophylaxis of influenza A virus infection. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 1777 BP; 565 A; 363 C; 420 G; 429 T; 0 U; 0 Other;

Query Match 57.2%; Score 607.2; DB 2; Length 1777;
Best Local Similarity 74.0%; Pred. No. 6.3e-161;
Matches 784; Conservative 0; Mismatches 273; Indels 3; Gaps 1;

QY 5 AAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCACTATTATTTTGTATCTACTGACCCA 64
DB 12 AAAGCAGGGGATATTTCTATTAATCATGAAGACCATCTTGTCTTGTAGCTATATTTCTG 71
QY 65 TTGGGTCTACAGTCAAAAC---CAAACCACTGGAAACAAACACAGCCACATTAATGTCTGGG 121
DB 72 TCTGGCTCTCGGCCAAGACCTTCCAGGAATGACAACAGCAGCAGCAGCTGTGCTGGG 131
QY 122 ACACCATGCTAGCAATGGACATTTGTAATAACATTAATCACTGATGACCAATTTAGGT 181
DB 132 ACATCATGCGGTGCCAAACGGAACACTAGTGAACAAATCACAGATGATCAGATTGAAGT 191
QY 182 GACAAATGCTACTGAATTTAGTTCAGAGCATTTCAATAGGGAATAATGCAACAACTCATA 241
DB 192 GACTAATGCTACTGAGCTAGTTAGAGCTCTCAACGGGGAATAATGCAACAACTCTCA 251
QY 242 TAAAGTTCTAGATGGAGAAATTCACATTAATAGATGCAATCTAGGAGACCCCACTG 301
DB 252 TCGAATCTTGTAGTAAGTACACTGACATGATAGTCTTATTTGGGGACCTCATTTG 311
QY 302 TGATGCTTCCAGTATGAGAATTTGGGACCTTCTATAGAAAGAGCAGCGCTTTACGAA 361
DB 312 TGATGTTTTTCAAAATGAGACATGGGACCTTTTCGTGAAACGAGCAAAAGCTTTACGAA 371
QY 362 TTGCTACCCATATGACATCCTGACTATGATGATCGCTCCGCTCCATTTGTAGCATCTCAGG 421
DB 372 CTGTTACCTTATGATGTCAGATTAATGCTCTCCCTTAGTCTAGTGTGCTCTGTCAGG 431
QY 422 AACATTAGAATTCACAGCAGAGGATTCACATGGACAGAGGTGTCACTCAAAACGGAAGAAG 481
DB 432 CACTCTGGAGTTTATCACTGAGGTTTTCATCTTGGACTGGGTCCTCAGAAATGGGGAAG 491
QY 482 TGGAGCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTTGGCTAACAA 541
DB 492 CAATGCTTGCAAAAGGGGACCTGGTAGCGGTTTTTTCAGTAGACTGAACCTGGTTGACCA 551
QY 542 ATCTGGAACACTCTTACCCCACTTGAATGTGACAATGCTTAAACAATAAAAAATTTTCGACA 601

DB 552 ATCAGGAGCACATATCCAGTCTGAACTGACTATGCCAAACATGACAAATTTTGACAA 611
QY 602 ACTATACATCTGGGGATTTCATCCCGAGCTCAACCAACAGCAGACAGAAATTTGACAT 661
DB 612 ACTATACATTTGGGGATTTCACACCCGAGCAGAAACCAAGAACAAACCCGCTGTATGT 671
QY 662 CCAAGNAATCAGGACGAGTAACAGTCTCAACAAAGAGAGTCAACAAACGATAGTCCCTAA 721
DB 672 TCAAGCATCAGGAGAGTCAAGTCTCTACAGGAGAGCCAGCAAACTATATATCCGAA 731
QY 722 TATCGGATCTAGACCGTGGTTAGGGGTCAATCAGCAGGATAAGCATATCTTGGACCAT 781
DB 732 TATCGGTCACAGCCCTGGGTAAAGGGTCTGTCTAGTAGAATAAGCATCTATTGGACAAT 791
QY 782 TGTAAACCTCGAGATATCTTAATGATAACAGTAATGCAACTTAGTTGGACCGCGGG 841
DB 792 AGTTAAGCCGGGAGAGCTACTGCTAATTAATAGTAATGGAAACCTAATCGCTCTCGGG 851
QY 842 ATATTTTAAATTTGAAACAGGGAAGCTCTCTAATGAGATCAGATGCAACCCATAGACAT 901
DB 852 TTATTTCAAAATGCGCACCTGGGAAAGCTCAATAATGAGTCAAGTGCACCTATTGATAC 911
QY 902 TTGTGTCTGTAATGATTATACACCAATGGAAGCTCTCCCAACGACAAACCACTTTCAAAA 961
DB 912 CTGTATTTCTGTAATGATCACTCCAAATGGAAGCATTCCTCAATGACAAGCCCTTTCAAA 971
QY 962 TGTGAACAAAGTTTACATATGGAATAATGCCCAAGTATATCAGGCAAAACACTTTAAAGCT 1021
DB 972 CGTAAACAGATCACATATGGAGCATGCCCAAGTATGTTAAGCAAAACACCCCTGAAGTT 1031
QY 1022 GGCCTCTGGATGAGGAATATACCAAGAAAGCAAACTAGA 1061
DB 1032 GGCAACAGGGATGCGGAATGTACAGAGAAACAAACTAGA 1071

RESULT 13
ABA93937
ID ABA93937 standard; DNA; 1765 BP.
XX
XX ABA93937;
XX AC
XX AC
XX 07-MAY-2002 (first entry)
XX
DE Influenza A/Udorn/72 (H2N2) Strain HA encoding DNA SEQ ID NO:7.
XX
XX Influenza A/Udorn/72 (H2N2) strain; Influenzavirus A; diagnosis;
KW Influenza A virus; genome; gene; ds.
XX
XX Influenzavirus A.
XX
XX Key Location/Qualifiers
FH CDS 30..1730
FT /*tag= a
FT /product= "HA protein"
XX
XX WO200200884-A2.
XX
XX 03-JAN-2002.
XX
XX 21-JUN-2001; 2001WO-US019826.
XX
XX 23-JUN-2000; 2000US-0213650P.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Galarza JM, Latham TE;
XX
XX WPI; 2002-139923/18.
DR P-PSDB; ABB05767.
XX
PT Polynucleotide encoding complete sequence of influenza A/Udorn/72 and
PT polypeptide, useful in diagnosis and for generating new influenza A

variant strains.

Claim 1; Page 61-64; 103pp; English.

The present invention describes an isolated polynucleotide (I) having the complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive strand, antigenomic message sense. ABA93944 to ABA93944 encode the Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to ABB05774 from the present invention. (I) is useful for designing polymerase chain reaction (PCR) primers for use in a PCR assay to detect the presence of the corresponding virus segment in a sample or for designing and selecting peptides for use in an enzyme linked immunosorbant assay to detect the presence of the corresponding protein produced by that segment in a sample, hence is useful in diagnosis and may be modified by mutation to generate new influenza A variant strains. ABA94945 to ABA94039 represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which are used in an example from the present invention

Sequence 1765 BP; 568 A; 355 C; 414 G; 428 T; 0 U; 0 Other;

Query Match 56.7%; Score 601.6; DB 6; Length 1765;

Best Local Similarity 73.5%; Pred. No. 2.4e-159;

Matches 782; Conservative 0; Mismatches 279; Indels 3; Gaps 1;

1 AGCAAAAGCAGGGGATATTTCTGTAATCATGAAGACAAACCATATTTTGTACTACTGA 60
1 AGCAAAAGCAGGGGATATTTCTGTAATCATGAAGACAAACCATATTTTGTACTACTGA 60
61 CCCATTGGTCTACAGTCAAAAC---CCAAACAGTGGAAACAAACACAGGCCACATTTATGTC 117
61 TCTGCTGGTCTCGGCGCAAACTTCCAGGAATATGACACAGCACAGCAACGCTGTGCC 120
118 TGGGACACCATGAGTACCAATGGAATGTTGTAATGTAATGTAATGTAATGTAATGTAATG 177
121 TGGGACATCATCGCGTCCAAACGACACACTAGTGAACAAATCACAATATGATCAGATTG 180
178 AGGTGACAAATGCTACTGTAATTTAGTTCAGAGCATTTTCAATAGGGAATATGCAACAACT 237
181 AAGTGACTAATGCTACTGAGTGTTCAGAGTCTCTCAACGGGGAATATGCAACAACT 240
238 CATATAAGTTCTAGATGGAAGAAATGACATTAATAGATGCAATGCTAGGAGACCCCC 297
241 CTCATCAATCTTGTAGTGAATAGTGCACACTGATAGATGCTTCTATTGGGGACCCCTC 300
298 ACTGTGATGCTTCCAGTATGAGAAATGGGACCTTTTCATAGAAGAGCAGCGCTTCA 357
301 ATTGTGATGGCTTTCAAAATGAGACATGGGACCTTTTCGTGAAACGACGACAAAGCTTCA 360
358 GCAATGCTACCCATATGATCCTGACTATGATGCTCGCTCGGTCCTATTGTAGCATCCT 417
361 GCACTGTATCCCTTATGATGTCGACATATGCTCTCCTTAGTCTAGTCTAGTCTGCTCGT 420
418 CAGGAAATATAGAAATCAGCAGAGAGGATTCATGACAGAGGTGTCACCTCAAAACGGAA 477
421 CAGGCACTCTGGAGTTTATCAGTGAAGGCTTCACTTGGACTGGGGTCACTCAGAAATGGG 480
478 GAGTGAGGCTGCAAAAGGGATCAGCCGATGTTCTTTAGCCGACTGAATTTGGCTAA 537
481 GAAGCAATGCTTCAAAAGGGGACCTGATAGCGGTTTTTTTTCAGTAGACTGAATTTGGT 540
538 CAAATCTGGAACCTTTTACCCCAATTTGATGTAATGTAATGTAATGTAATGTAATGTAATG 597
541 ACAATCAGGAGCAGATATCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
598 ACAATCTATATCTGGGGATTCATCACCAGGCTCAAAACCAACAGCAGACAGAAATTTGT 657
601 ACAATCTATATCTGGGGATTCATCACCAGGCTCAAAACCAACAGCAGACAGAAATTTGT 660
658 ACATCCAGAAATCAGGAGAGTATCAGTCTCAACAAAAGAGTCAACAAACAGTATGTC 717
661 ATGTTCAAGCATCAGGGAGATGTCACAGTCTCTTACCAAGAGAGCGCAACAAATATATCC 720
718 CTAATATCGGATCTAGACCGTGGGTAGGGGTCAATCAGGAGGATGAATGATATCTACTGGA 777

721 CGAATATCGGGTCTAGACCTCGGTAAAGGGTCTGTCTAGTAGAATAAGCATCTATTGGA 780
778 CCATTGTAAACCTGGAGATATCTTAATGATAAAGCACTTAATGGCACTTAGTTGACCGC 837
781 CAATAGTTAAACCGGGAGACATATCTGTAATTAATAGTAATGGGAACCTAATTTGCTCCTC 840
838 GGGGATATTTTAAATGAAAACAGGGGAAAGCTCTGTAATGAGATCAGATGCAACCCATAG 897
841 GGGGATATTTTAAATGCGGCACTGGGAAAGCTCAATATGAGTCAAGTGCACCTATTG 900
898 ACATTTGTGTCTGTAATGTAATACCAATGGAAGCATCCCCAAGCAACAAACCATTTTC 957
901 GCACCTGCACTTTCTGTAATGATCATCTCCAAATGGAAGCATTTCCCAATGACAGCCCTTTC 960
958 AAAATGTGAACAAAGTTACATATGGAATAATGCCCCAAGTATATCAGGCAACAAACATTTAA 1017
961 AAAACGTAACAAAGATCAGATATGGGCACTGTCCCAAGTATGTTAAGCAAAACACCCCTGA 1020
1018 AGCTGGCCACTGGGATGAGCAATATACCAAGAAAGCAAAATCAGA 1061
1021 AGTTGGCAACAGGATGCGGAATGTACCAAGAAACAAACTAGA 1064
RESULT 14
ABA93944
ID ABA93944 standard; DNA; 1764 BP.
XX ABA93944;
XX AC
XX XX
DT 07-MAY-2002 (first entry)
XX
DE Influenza A/Udorn/72 (H3N2) Strain HA encoding DNA SEQ ID NO:21.
XX
XX Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
XX Influenza A virus; genome; gene; ds.
OS Influenzavirus A.
FH Key Location/Qualifiers
FT CDS 30..1730
FT /*tag= a
FT /product= "HA protein"
XX
PN WO200200884-A2.
XX
XX 03-JAN-2002.
XX
XX 21-JUN-2001; 2001WO-US019826.
XX
XX 23-JUN-2000; 2000US-0213650P.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Galarza JM, Latham TE;
XX
XX WPI; 2002-139923/18.
XX P-PSDB; ABB05774.
XX
XX Polynucleotide encoding complete sequence of influenza A/Udorn/72 and
XX variant strains.
XX
XX Claim 1; Page 80-83; 103pp; English.
XX
XX The present invention describes an isolated polynucleotide (I) having the
XX complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive
XX strand, antigenomic message sense. ABA93944 to ABA93944 encode the
XX Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to ABB05774
XX from the present invention. (I) is useful for designing polymerase chain
XX reaction (PCR) primers for use in a PCR assay to detect the presence of
XX the corresponding virus segment in a sample or for designing and
XX selecting peptides for use in an enzyme linked immunosorbant assay to

CC detect the presence of the corresponding protein produced by that segment
CC in a sample, hence is useful in diagnosis and may be modified by mutation
CC to generate new influenza A variant strains. ABA94945 to ABA94039
CC represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which
CC are used in an example from the present invention
XX

SQ Sequence 1764 BP; 568 A; 355 C; 414 G; 427 T; 0 U; 0 Other;

Query Match 56.4%; Score 598.4; DB 6; Length 1764;
Best Local Similarity 73.3%; Pred. No. 1.9e-158;
Matches 780; Conservative 0; Mismatches 281; Indels 3; Gaps 1;

QY 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAGACAACCACTATTATTTGATCTACTGA 60
DB 1 AGCAAAAGCAGGGGATATTTCTATTAACCATGAAGAACTATCATTTGCTTGAGCTACATTT 60
QY 61 CCATTTGGGTCTACAGTCAAAAC---CCAAACAGTGGAAACAACACAGCCACATTTATGTC 117
DB 61 TCTGTCTGTGTTCTCGGCCAAGACTTTCCAGGAATGACAACAGCAGCAACGCTGTGCC 120
QY 118 TGGGACACCATGAGTAGCAATGGACATTTGCTTAAACAATAAATGATGACCAATTTG 177
DB 121 TGGGACATCATGCGGTGCCAAACGGAACACTAGTGAACAATCAAAATGATCAGATTG 180
QY 178 AGGTGACAAATGCTTACTGAATTAGTTTCAGAGCATTTCAATAGGGAATAATGCAACAAC 237
DB 181 AAGTGACTAATGCTACTGAGTGTTCAGAGTTCTCTCAACGGGGAATAATGCAACAATC 240
QY 238 CATATAAAGTTCTAGATGGAAGAAATGACATTAATAGATGCAATGCTAGGAGACCC 297
DB 241 CTCATCGAATCCTTGATGGAATGAGCTGACACACTGATAGTCTCTATTGGGGGACCC 300
QY 298 ACTGTGATGCTTCCAGTATGAGAAATTTGGGACCTCTTCATAGAAAGAGCAGCGCTTCA 357
DB 301 ATTGTGATGCTTTCAAAATGAGACATGCGACCTTTTCGTTGAACGAGCAAAAGCTTTCA 360
QY 358 GCAATTTGCTACCATATGACATCCCTGACTATGATGCTCGGTCCGTTCCATTTGTAGCATCCT 417
DB 361 GCAACTGTTTACCCTTATGATGTCCAGATTATGCTTATGCTTACCTAGTGTGCTCGT 420
QY 418 CAGGAACATTAGAAATTCACAGCAGAGGGATTACATGGACAGTGTCTACCAAAACGGAA 477
DB 421 CAGGCATCTCGAGTTTATCAGTGAAGGCTTCTCTTGGACTGGGGTCACTCAGAAATGGG 480
QY 478 GAAGTGGAGCTGCAAAAGGGGATCAGCGATAGTTTCTTTAGCCGACTGAATTTGCTAA 537
DB 481 GAAGCAATGCTTGCAAAGGGGACCTGATAGCGGTTTTTTCAGTAGACTGAACTGGTTGT 540
QY 538 CAAAATCTGGAAACTCTTTACCCACATTTGAATGTGCAATGSCCTTAACAATAAATAATTCG 597
DB 541 ACAATCAGGAAGCACATATCCAGTGTGAACGTGACTATGCCAAACATGACAATTTTG 600
QY 598 ACAACATATACATCTGGGGATTCATCACCGAGTCTAAACCAACAGAGACAGAAATGT 657
DB 601 ACAACATATACATTTGGGGGTTTCACACCCGAGCAGCGGACCAAGAACCAACAGCGCTAT 660
QY 658 ACATCCAAGAAATCAGGACGAGTAACAGTCTCAACAAAGAAAGTCAACAAACATAGTCC 717
DB 661 ATGTTTAGCATCAGGGAGAGTCAAGTCTCTACCAAGAGAACCGAACAATATATATCC 720
QY 718 CTAATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGACAGGATAAGCATATACTGGA 777
DB 721 CGAATATCGGGTCTAGACCTGGGTAAGGGTCTGTCTAGTAGAATAAGCATCTATTGGA 780
QY 778 CCATTGTAAACCTGGAGATATCCTAATGATAACAGTAAATGCAACTTAGTTGACCCG 837
DB 781 CAATAGTAAACCGGGAGACATATCTGGTAATTAATAGTAATGGAACCTTAATTTGCTCCT 840
QY 838 GGGGATATTTAAATTTGAAACAGGGGAAAGCTCTGTAAATGAGATCAGATGCAACCCATAG 897
DB 841 GGGGTTATTTAAATGCGGACCTGGGAAAGCTCAATATAGGTGAGTGCACCTATTG 900
QY 898 ACATTTGTGTGTGAATGATTATACACCAAAATGGAAGCATCCCCAACAGCAAAACCAATTC 957

DB 901 GCACCTGCATTTTCTGAATGCATCACTCCAAATGGAAGCATTCCTCAATGACAAGCCCTTTC 960
QY 958 AAAATGTGACAAAGTTTACATATGGAATGCCCCAAGTATATCAGGCAAAACACTTTAA 1017
DB 961 AAAACGTAAACAAGATTCACATATGGGGCATGTCCCAAGTATGTTAAGCAAAACACCTGA 1020
QY 1018 AGCTGGCCACTGGGATGAGGAATATATACAGAAAAGCAAAATCAGA 1061
DB 1021 AGTTGGCAACAGGATGCGGAATGTACCAAGAAACAAACTAGA 1064

RESULT 15

AAN70642

ID AAN70642 standard; cDNA; 1762 BP.

XX AAN70642;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 29-APR-1991 (first entry)

XX Sequence encoding influenza HA protein.

XX HA; vaccine; ds.

XX Influenza A virus; 'A/Niigata 102181'.

XX JP62051992-A.

XX 06-MAR-1987.

XX 30-AUG-1985; 85JP-00192915.

XX 30-AUG-1985; 85JP-00192915.

XX (KAGA) KAGAKU KASEI RYOHO KENKYUSHO.

XX WPI; 1987-104909/15.

XX Recombinant plasmid - combines influenza virus gene and transformation enzyme and can be used for prepn. of influenza virus protein.

XX Disclosure; Fig 3; 14pp; Japanese.

XX Sequence may be inserted into a plasmid under the control of a

CC phosphatase promoter, and used to transfer an E.coli expression system.

CC The HA protein product may be used as vaccine against influenza viral

CC infection. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-

CC AUG-2003 to correct OS field.)

XX Sequence 1762 BP; 579 A; 359 C; 404 G; 420 T; 0 U; 0 Other;

Query Match 55.2%; Score 585.6; DB 1; Length 1762;

Best Local Similarity 72.6%; Pred. No. 8e-155;

Matches 772; Conservative 0; Mismatches 289; Indels 3; Gaps 1;

QY 1 AGCAAAAGCAGGGGATATTTCTGTCATCATGAGACAACCACTATTATTTGATCTACTGA 60

DB 1 AGCAAAAGCAGGGGATATTTCTATTAAACCATGAGACTATCATTTGCTTTGAGTCAATTT 60

QY 61 CCATTTGGGTCTACAGTCAAAAC---CCAAACAGTGGAAACAACACAGCCACATTTATGTC 117

DB 61 TCTGTGAGTTCTCGCCCAAAACCTTCAGGAAATGACAACAGCAGCAACGCTGTGCC 120

QY 118 TGGGACACCATGAGTAGCAAAATGGAACATTTGGTAAAAACAATACTGATGACCAATTTG 177

DB 121 TGGCAGCATGATGTAGTGCACCAACGGAACGCTAGTGAACCAATCAGGAATGATCAGATTG 180

QY 178 AGGTGACAAATGCTACTGAAATTTAGTTTCAGAGCATTTCAATAGGGAATAATGCAACAAC 237

DB 181 AAGTGACTAATGCTACTGAGTGGTTTCAGAGTTCTTCAACAGTAGAATATGCGACATC 240

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 03:19:06 ; Search time 4183 Seconds
(without alignments)
11867.343 Million cell upda

Title: US-10-826-929A-1
 Perfect score: 1061
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Scoring table: IDENTITY NUC

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:★

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3: gb_est3:*
4: gb_hlc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	44.6	4.2	878	10	CNS0187R	AL108993	Drosophil
2	43.8	4.1	598	9	AQ636729	RPCI-11-4	AQ636729
C 3	43.8	4.1	820	9	CC081372	CSU-K33r.	CC081372
C 4	42.8	4.0	854	10	CNS0090S	AL052980	Drosophil
5	42.4	4.0	1101	10	CNS0106X	AL098595	Drosophil
C 6	42.2	4.0	1199	8	DN707481	CLJ71-G04	DN707481
7	42	4.0	665	5	BY725844	BY725844	BY725844
C 8	41.6	3.9	1106	10	CNS00LRE	AL078634	Drosophil
C 9	41.4	3.9	733	9	AQ055729	CIT-HSP-2	AQ055729
10	41	3.9	1101	10	CNS00H6Y	AL073010	Drosophil
C 11	41	3.9	1362	10	AG429915	Mus muscu	AG429915
C 12	40.8	3.8	750	8	CX894805	AG29915	Mus muscu
C 13	40.8	3.8	879	5	EX693295	JGI CARM6	EX693295
C 14	40.8	3.8	1342	10	CL650318	CH213-288	CL650318
15	40.6	3.8	503	9	BH744818	gt42405.b	BH744818
C 16	40.6	3.8	643	7	CK563538	rswpb0.00	CK563538
C 17	40.6	3.8	968	10	CNS0172G	AL107506	Drosophil
18	40.4	3.8	1005	9	AZ345336	1M0079P14	AZ345336
C 19	40.4	3.8	105	10	CNS007DW	AL067043	Drosophil
C 20	40.2	3.8	470	7	CK747765	nad03-4cs	CK747765
C 21	40	3.8	588	10	AG972417	Drosophil	AG972417
22	39.8	3.8	568	10	CW303050	104 787.1	CW303050

ALIGNMENTS

RESULT 1	CNS0187R	878 bp	DNA	linear	GSS 26-JUL-1999
CNS0187R	Drosophila melanogaster genome survey sequence SP6 end of BAC				
LOCUS	BACN04E04 of DrosBAC library from Drosophila melanogaster (fruit				
DEFINITION	flv), genomic survey sequence.				

ACCESSION NUMBER	VERSION	KEYWORDS	SOURCE	ORGANISM
AL108993	1	GI:5629297	GSS.	<i>Drosophila melanogaster</i> (fruit fly)
AL108993.1				<i>Drosophila melanogaster</i>
				<i>Drosophila melanogaster</i>
				Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyraeidea; Drosophilidae; Drosophila

1 (bases 1 to 878)
Genoscope.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT 1
determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) <http://www.edgp.ebi.ac.uk>. This *Drosophila melanogaster* BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Pavan. It has been constructed in the vector

FEATURES	source	Location/Qualifiers
pBelOBAC11.		
		1..878
		/organism="Drosophila melanogaster"
		/mol_type="genomic DNA"
		/db_xref="taxon:7227"
		/clone="BACN04E04"
		/clone_lib="DrosBAC"
		/plasmid="pBelOBAC11"
		/note="end : SP6"

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Query Match          4.2%; Score 44.6; DB 10; Length 878;
Best Local Similarity 24.1%; Pred. No. 0.84;
Matches 62; Conservative 83; Mismatches 112; Indels 0; Gaps 0;

QY 762 ATAAGCATATACTGGACCACTGTAATAACCTGGAGATCTCTAATAACAGTAATGCC 821
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 93 AWAAMAMWMAAAMMAAMWMAWGAWGWGAWMMWMAWGMWMAWMAAAMMAA 152

QY 822 AACTTACTTGACCGCGGGATATTTTAAATTTGAAAACAGGGAAGCTCTGTAAATGAGA 881

Db 153 WMMWCTTTGCMCTGAWTRTWGTRTWAWWMTTAAAWWMAWMAWMAWMAWMAW 212

QY 882 TCAGATGACCCCATAGACATTTGTGTCTGGAATGTATTAACACAAATGGAAGCATCCCC 941

Db 213 WWRGMAAARAAMWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAW 272

QY 942 AACGACAAACATTTCAAAATGTGAACAAAGTTACATATGGAATGCCCAAGTATATC 1001

Db 273 MAAMWCCAAWVGGAFAAATWGAWMMWMAWMAAAMRAARMWMAWMAWMAWMAWMA 332

QY 1002 AGGCAAAACACTTTAAA 1018

Db 333 CAWAAWAAARTWRTA 349

RESULT 2
AO636729 598 bp DNA linear GSS 17-JUN-1999

LOCUS
DEFINITION
RPCI-11-477P23-TV RPCI-11 Homo sapiens genomic clone

ACCESSION
AO636729

VERSION
AO636729.1 GI:5099364

KEYWORDS
GSS.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
1. (bases 1 to 598)

AUTHORS
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

TITLE
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

JOURNAL
Unpublished (1997)

COMMENT
Other GSSs: RPCI-11-477P23.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@igr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: T7

Class: BAC ends.

FEATURES
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/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/notes="Vector: pAc3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

ORIGIN

Query Match 4.1%; Score 43.8; DB 9; Length 598;
Best Local Similarity 56.4%; Pred. No. 1.3;
Matches 101; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 100 ACACAGCCACATTATGTCTGGGACACCATGAGTAGCAATGGAACATTGGTAAAAACAA 159

Db 198 ATATAGCAGAAACACATTTATGACACGATTACATTATACAGAAAATGTTGACTAAAGAA 257

QY 160 TAACTGATGACCAAAATGAGGTGACAAATGCTACTGAATTAGTTGAG-AGCATTTCATA 218

Db 258 TAACCAATTTAAAAAATTTGAAGAGTGAATTTTAAATTAATTCAGTAAAAAGTACGAGA 317

QY 219 GGGAAAATATGCAACAACATCATATAAAGTTCTAGATGGAAGAAATTCGCATTAAATAGA 277

Db 318 TGTAGAATATGAACAAATTTATATTAATTAATAAGAAACATTGTCTTAAATATA 376

RESULT 3
CC081372/c 820 bp DNA linear GSS 16-APR-2003

LOCUS
DEFINITION
CSU-K33r.31E9.SP6 CSU-K33r Aedes aegypti genomic clone

ACCESSION
CC081372

VERSION
CC081372.1 GI:29929272

KEYWORDS
GSS.

SOURCE
Aedes aegypti (yellow fever mosquito)

ORGANISM
Aedes aegypti

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Culicinae; Culicini; Aedes; Stegomyia.

REFERENCE
1. (bases 1 to 820)

AUTHORS
Loftus,B., Shetty,J., Severson,D., Brown,S. and Knudson,D.

TITLE
End sequencing of Aedes aegypti BACs

JOURNAL
Unpublished (2003)

COMMENT
Other GSSs: CSU-K33r.31E9.T7
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by Susan Brown and Dennis Knudson at Colorado State University.
Seq primer: SP6
Class: BAC ends.

FEATURES
source
1..820
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/clone_lib="CSU-K33r"
/note="Vector: pBelobAC11; Site_1: HindIII"

ORIGIN

Query Match 4.1%; Score 43.8; DB 9; Length 820;
Best Local Similarity 49.0%; Pred. No. 1.4;
Matches 117; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 42 ATTATTTGATACTACTGACCCATTTGGGTCTACAGTCAAAACCCACCACTGGGAACAAC 101

Db 284 ATCATTTCAAACCTGTGTTTTCCGTAGTTACACGGAAATAAATAACGCTCCGAAAAAA 225

QY 102 ACAGCCACATTTATGTCCTGGGACACCATGCGATGAGCAATGGAAATTCGTTAAAAACAATA 161

Db 224 AAATAAAATTTAAATATTTTAAATAACCGAAACAATTTGAAATTTTATTTATTTGCCAAA 165

QY 162 ACTGATGACCAATTTAGGTGACAAATGCTACTGAATTTAGTTTCAGAGCATTTCAATAGGG 221

Db 164 AATCAACAACCTAGAAAAGGCTTCAGAAAAAATGAAAAAGCTAGGGATGTTCAAAAAATA 105

QY 222 AAAAATATGCAACAACATCATATAAAGTTCTAGATGGAAGAAATTCGCACATTAAATAGATGC 280

Db 104 AAATTTATAAAATCAAAAACCAAAATTTAAAAATTTTGTAATAAAAAATTAATAATGC 46

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RESULT 4
CNS00905/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR19H07 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
VERSION
AL052980
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoss in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
Location/Qualifiers
1. .854
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR19H07"
/clone_lib="RPCI-98"
/notes="end : T7"
FEATURES
source
ORIGIN
Query Match 4.0%; Score 42.8; DB 10; Length 854;
Best Local Similarity 30.3%; Pred. No. 2.6; Mismatches 358; Indels 3; Gaps 1;
Matches 158; Conservative 2;
Qy 536 AACAAATCTGGAACCTTTACCCACACATTGAATGTGACAACTGCTAACCAATAAAAAATTT 595
Db 626 AANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 567
Qy 596 CGACAAACTATACATCTGGGGGATTCTACCCGAGTCTCAACCAACAGCAGACAGAAAT 655
Db 566 AANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 507
Qy 656 GTACATCAAGATCAGACAGGTAACAGTCTCAACAAAGAGTCAACAAACGATAGT 715
Db 506 NNAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 447
Qy 716 CCCTAATATCGGATCTAGACCGTGGGTGAGGTGCAATCGAGCAGGATAAGCATATAGT 775
Db 446 NNAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 390
Qy 776 GACCATTTGTAACCTGGAGATATCTTAATGATATAACAGTAATGGCACTTAGTTCACC 835
Db 389 NNAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 330
Qy 836 GCGGGGATATTTAAATTTGAACAGGGAAGAGCTCTGTAATGAGATCAGATGCCCAT 895
Db 329 NANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 270
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896 AGACATTTGTGTCTGAATGTATTACACCAAAATGGAAGCATCCCAACGACAAACCAT 955
269 ANNNANATNNNNAAGNNTANNANNAANAANAANAANAANAANAANAANAANAANA 210
956 TCAAAATGTGAACAAAGTTACATATGGAATATGCCCAAGTATATATCAGGCAAAACATTT 1015
209 NNNNNAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 150
1016 AAAGCTGCCACTGGGATGAGGATATACACGAAACGAA 1056
149 NNNNCADVKAACCAAAAGGAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 109
CNS0106X 1101 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN03K20 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
VERSION
AL098595
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaut at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.
Location/Qualifiers
1. .1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN03K20"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/notes="end : T7"
FEATURES
source
ORIGIN
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Best Local Similarity 19.3%; Pred. No. 3.7;
Matches 67; Conservative 140; Mismatches 141; Indels 0; Gaps 0;
Qy 563 ATTGAATGTGACAATGCCTAACCAATAAATTTTCGCAAACTATACATCTGGGGGATTC 622
Db 754 RDKRRWDKDKKRRKAKAKAAADADADADAKADAKADAKADADADGRGDGKKRA 813
Qy 623 TCACCCGAGCTCAACCAACAGCAGACAGAAATTTGTATCATCCAAAGATTCAGACGAGTAAC 682
Db 814 KDRKKKKKKDKWGDKKKKKKDKKAAKADAAAGDAKAKERRRAGDKDKADAKAKAKAK 873
Qy 683 AGTCTCAACAAAAGAGTCAACAAACGATAGTCCCTTAATATCGGATCTTAGACCGTGGT 742
Db 874 AKDDDDAKAATKAKATKAKKDKAKAKKKKKDKDKAKAKAKADKDKDDDDKDDKK 933
Qy 743 TAGGGTCAATCAGGAGGATAGCATATATCTGGAACCATTTGTAAAACCTGGAGATATCT 802
Db 934 DAKADKKKKKKDKKDKKDKKDKKDKKDKKDKKDKKDKKDKKDKKDKKDKKDKK 993
Qy 803 AATGATAAAACAGTAATGGCAACTTAGTTGACCGCGGGGATATTTTAAATTTGAAACAGG 862
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	Matches	87; Conservative	0; Mismatches	76; Indels	0; Gaps	0;
Qy	129	GCAGTAGCAAAATGGACATTGTTAAAAACAATAACTGATGCCAAATTCGAGGTGACAAAT	188			
Dd	469	GCAGCAGGAATGAAATGATAGATTAAATTAAGAAGAGAAAATATCAATAGTAGTTTT	410			
Qy	189	GCTTACTGAATTAGTTTCAGAGCACATTTCAATAGGGAAAAATATGCACCAACTCATATAAAGTT	248			
Dd	409	TAAATAAATATGTTTCAGAAATCTGAAGGGTAAAAAATGAATAATCCATAAAGGAA	350			
Qy	249	CTAGATGGAGAANTTGCACTTAATAGATGCATGCTAGGAG	291			
Dd	349	CAAGAATTATGAACATAAACGCAGATTAAATGAAATAATAAAG	307			
RESULT 10	CNS00H6Y	1101 bp	DNA	linear	GSS 03-JUN-1999	
LOCUS	Drosophila melanogaster genome survey sequence T7 end of BAC:					
DEFINITION	BACR34L01 of RPECI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.					
ACCESSION	AL073010					
VERSION	AL073010.1 GI:4952872					

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 1101)	Drosophila melanogaster	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
		Genoscope.		
		Direct Submission		
		Submitted (02-JUN-1999)	Genoscope - Centre National de Sequencage :	
		BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
		- Web : www.genoscope.cns.fr)		
		Determination of this BAC-end sequence was carried out as part of a		
		collaboration with the Berkeley Drosophila Genome Project (BDGP).		
		The BDGP is constructing a physical map of the Drosophila		
		melanogaster genome using these BACs. For further information		
		please see http://www.fruitfly.org The BDGP Drosophila		
		melanogaster BAC library was prepared by Kazutoyo Ooeogawa and		
		Aaron Mammoser in Piter de Jong's laboratory in the Department		
		Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,		
		NY. The library is named RP01-98 and was constructed by partial		
		EcoRI digestion of Drosophila DNA provided by the BDGP from the		
		isogenic strain Y2; cn bw sp, the same strain used for the BDGP's		
		F1 and EST libraries. A more detailed description of the library		
		and how to order individual BAC clones, the entire library, or		
		filters for hybridization from the BACPAC Resource Center can be		
		found at http://bacpac.med.buffalo.edu/drosophila/bac.htm .		

ORIGIN		Query Match	3.9%;	Score 41;	DB 10;	Length 1101;	
		Best Local Similarity	43.1%;	Pred. No. 8.9;			
		Matches 119;	Conservative 13;	Mismatches 144;	Indels 0;	Gaps 0;	
Qy	79	AAACCCGACCGTGGAAACACACAGCCACCATTTGTC					138
Db	302	AACCCCGATCCCAATCAATCAATGCTTACATATAAATTTAACTAAT					361
Qy	139	ATGGAACATCTGTTAAAAACAATAACTGATGACCAAAATTTGAGGTG					198
Db	362	TACAAACAANAACCAAAWATATTTTATATATATAAATATAWATATW					421
Qy	199	TAGTTTCAGAGCATTTTCAATATAGGGAATAATGCAACAACATCATATA					258

This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn. cDNA was oligo dT primed from 5' of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end. Vector: pCS107; Site 1: EcoRI; Site 2: NotI. Host: *Escherichia coli* DH10B.

the clone was

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